us-10-040-647-6.rup

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SEQUENCE FROM N.A.
MEDLINE=20461760; PubMed=11000480; DOI=10.1016/S0167-4781(00)00071-3; MEDLINE=20461760; PubMed=11000480; DOI=10.1016/S0167-4781(00)00071-3; Hooper J.D., Dowen N., Marshall H., Cullen L.M., Sood R., Daniels R., Stuttgen M.A., Normyle J.F., Higgs D.R., Kastner D.L., Ogbourne S.M., Pera M.F., Jazwinska E.C., Antalig T.M.; "Localization, expression and genomic structure of the gene encoding the human serine protease testisin."; "Biochim. Biophys. Acta 1492:63-71(2000).
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MEDLINE=22887296; PubMed=1275309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
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               GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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TISSUE=Ecainophil;
MEDLINE=99045401; PubMed=9826525; DOI=10.1006/bbrc.1998.9645;
Inoue M., Kanbe N., Kurosawa M., Kido H.;
"Cloning and tissue distribution of a novel serine protease esp-1 from human ecsinophils.";
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Q9X6MO, Q9NS34; Q9P2V6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Testisin precursor (EC 3.4.21.-) (Bosinophil serine protease 1) (ESP-1) (UNQ26/PRO303).
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MEDLINE-99323395; PubMed=10397266;
Hooper J.D., Nicol D.L., Dickinson J.L., Eyre H.J., Scarman A.L.,
Normyle J.F., Stuttgen M.A., Douglas M.L., Loveland K.A.,
Sutherland G.R., Antalis T.M.;
Testisin, a new human serine proteinase expressed by premeiotic
testicular germ cells and lost in testicular germ cell tumors.";
Cancer Res. 59:3199-3205(1999).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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RSY4 MOUSE
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charge relay system (Potential).
Charge relay system (Potential).
Charge relay system (Potential).
Potential.
Potential.
Potential.
Potential.
GPI-anchor amidated serine (Potential).
N-linked (GICNAC. . .) (Potential).
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanbe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.; The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: Genome Res. 13:2265-2270(2003).

-!- FUNCTION: Could regulate proteolytic events associated with testicular germ cell maturation.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Removed in mature form (Potential)
                                                                                                                                                                                                                                                                                                                                                                       Isoid=Q9Y6M0-3; Sequence=VSP_005390;
-!- TISSUB SPECIFICITY: Expressed predominantly in premeiotic testicular germ cells, mostly late pachytene and diplotene spermatocytes.
-!- SIMILARITY: Belongs to the peptidase SI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERMYS; PRO0089; Trypsin, I.
PRINTS; PRO0722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN HIS; I.
PROSITE; PS00135; TRYPSIN BR; I.
Alternative splicing; Glycoprotein; GPI-anchor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN, busider, C:cytoplasm, TAS.
GO, GO:0005624; C:cytoplasm, TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0008886; C:plasma membrane; TAS.
GO; GO:0008286; F:serine-type peptidase activity; TAS.
InterPro; IPR001031; Pept Ser Cys.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                          (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyme=1; Sequence=Displayed;
Name=2; Synonyme=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease; Signal; Zymogen.
19 Potential.
                                                                                                                                                                                                                                                                                                                                  IsoId=Q9Y6M0-2; Sequence=VSP_005389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Testisin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF058300; AAD41588.1; --
EMBL; AB031329; BAA83220.1; --
EMBL; AB031331; BAA89532.1; --
EMBL; AF058301; AF79019.1; --
EMBL; AF058301; AAF79020.1; --
EMBL; AF058301; AAF79020.1; --
EMBL; AF058301; AAF79020.1; --
HSSP; P00734; AGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:9485; PRSS21.
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289
289
82
137
238
67
171
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PROPEP
ACT SITE
ACT SITE
ACT SITE
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDFSGWWQFGQLTSMPSFWSLQAYYTRYF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFBFBNRTDCWVTGWGYIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/Sv; MEDLINE=21153229; PubMed=11231276; Strain M.-L., Webb G.C., Scarman A.L., Hooper J.D., Boucaut K.J., Sit M.-L., Webb G.C., Normyle J.F., Antalis T.M.; Antalis T.M.; "Organization and chromosomal localization of the murine Testisin gene encoding a serine protease temporally expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PLACNKNGLMYQIGVVSWGVGCGRPNRPGVYTNISHHFEMIQKLMAQSGMSQPDPSWPLL
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STRAIN=BALB/C; TISSUE=Testis;
STRAIN=BALB/C; TISSUE=10.1074/jbc.M010422200;
PubMed=11259427; DOI=10.1074/jbc.M010422200;
WONG G.W., Li L., Madhusudhan M.S., Krilis S.A., Gurish M.F.,
Rothenberg M.E., Sali A., Stevens R.L.;
"Tryptase 4, a new member of the chromosome 17 family of mouse serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
                                                                                                                                                                                                                                                                                                                                                                                             1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
Missing (in isoform 2).
/FTIG=YSP_005389.
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                              Length 314;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                          /FTId=VSP 005390.
34884 MW; E738CF73F6B56E98 CRC64;
                                                                                                                Missing (in isoform 3).
                                                                                                                                                                                                                           Score 1723; DB 1;
Pred. No. 1.8e-145;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      090HJ7; Q9DR14;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
Testisin precursor (EC 3.4.21.-) (Tryptase 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spermatogenesis.";
Bur. J. Biochem. 268:1250-1258(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Biol. Chem. 276:20648-20658(2001).
                                                                                                                                                                                                                           Query Match 99.7%;
Best Local Similarity 99.7%;
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 FFPLLWALPLLGPV 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                   235
                                                                                                                                                                             314 AA;
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273
87
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Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Balla B., Dragani T.A., Fletcher C.F., Forrest A., Farzer K.S.,
Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Nagabinma T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Raid B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada Y., Walls C.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wanner L., Wahlestedt C., Wanny Y., Watanabe Y., Wells C.,
Willming L.G., Wynnehaw-Boris A., Yanagisawa M., Yang I.,
Vuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Milming L.G., Wanki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakasi K., Sasaki D., Shibata K., Shibata R.,
Miyazaki A., Sakasi K., Sasaki D., Shibata K., Shibata K.,
                                                                                                                                                                                                                                                                                                                                                                                                           Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Waterston R., Lander E.S., Rogers J., Hayashis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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(Potential). -1- TISSUB SPECIFICITY: Testis. -1- DEVELOPMENTAL STAGE: Expressed in post-meiotic testicular germ -!- FUNCTION: Could regulate proteolytic events associated with testicular germ cell maturation.

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-!- CAUTION: Ref.3 sequence differs from that shown due to a stop codon in position 315.

or send an email to license@isb-sib.ch).

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PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Glycoprotein; GPI-anchor; Hydrolase; Lipoprotein; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
Potential.
Testisin.
Removed in mature form (Potential).
EMBL; AF304012; AAK29360.1; -.
EMBL; AY005145; AAG2255.1; -.
EMBL; AF176209; AAF644207.2; -.
EMBL; AF256710; AAF64428.2; -.
EMBL; AK006271; -; NOT_ANNOTATED_CDS.
HSSP; P00734; IGHW.
MENOPS; S01.011; -.
MGI:1916689; Prss21.
GO; GO:0005624; C:membrane fraction; IDA.
GO; GO:0005525; F:serine-type endopeptidase activity; IDA.
InterPro; IPR001035; Pept. Ser Cys.
InterPro; IPR001035; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                     Pfam; PF00089; Trypsin; 1
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54
298
324
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Zymogen.
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Charge relay system (Potential).

CHAIN PROPEP ACT\_SITE

	4,	47	107	167	227	287		
Charge relay system (Potential). Charge relay system (Potential). Potential. Potential. Potential. Potential. Potential. Potential. N-linked (GLONAC) (Potential). P->H (in Ref. 3).	<pre>%; Score 1152; DB 1; Length 324; %; Pred. No. 1.9e-94; 38; Mismatches 60; Indels 16; Gaps</pre>	MGARGALILALLLARAGLRKPESOBAAPLSGPCGRRVITSRIVGGED	AELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMP 	SFWSLQAYYTRYFVSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFEN	RIDCWVIGWGYIKEDEALPSPHILQEVQVAIINNSMCNHLFLKYSFRKDIFGDNVCAGNA 	QGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQ 	LLWALPLIGP 313 	PRT; 336 AA. 24, Created) 24, Last sequence update) 26, Last annotation update)
147 147 248 248 248 167 96 96 96 181 254 233 298 298 298 177 177 177 210 210 2215 24 AA; 36175	66.78 Similarity 65.08 2; Conservative	MGARGALLLALLLAN         :    :  MGARGKTLVPLLVVVA	GRWPWQGSLRLWDS             GRWPWQGSLRVWGN	SLQAYYTRYFVSNI 	CWVTGWGYIKEDEA	KDACFGDSGGPLA(                  KDACFGDSGGPLA(	SGMSQPDPSWPLLFFPLLWALPLLGP : ::             NGLLRPDPVPLLLFLTLAWASSLLRP	PRELIMINARY; (TrEMBLrel, 24, (TrEMBLrel, 24, (TrEMBLrel, 26,
ACT_SITE ACT_SITE ACT_SITE DISULPID DISULPID DISULPID DISULPID CARBOHYD CAR	Query Match Best Local Simi Matches 212;	1 MGA	48 AEL/     61 AEL/	108 SFW       118 SLW	168 RTD     178 RTD	228 QGG :   238 EGG	288 SGM : : 298 NGL	LT 3 D8 Q80YD8 Q80YD8; 01-JUN-2003 01-JUN-2003
77777777777777777777777777777777777777	Our Ber Mat	\$ g	& g	& 8	λ <sub>O</sub> q <sub>O</sub>	\$ g	& 8	RESULT Q80YD8 ID Q AC Q DT 0 DT 0

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Colline F.S., Wagner L. Benemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz F. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Prss21 protein (Fragment).
                                         Mus musculus (Mouse)
                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Testis;
                                                                                                                      NCBI_TaxID=10090;
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45 GEDAELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 SMPSFWSLQAYYTRYFVSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 SRPSLWALQAYSNRYQIEDIFLSPKYTEQFPHDIALLKLSSPVTYSNFIQPICLLNSTYK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGARGALLLALLLARAGL--------RKPESQEAAPLSGPCGRRVITSRIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSARGKTLVPLLVVVVAVBVTLQSTSSHVKPVDPEKPELQEANLLSGPCGHRTIPSRIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 FENRTDCWVTGWGYIKEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNAQGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKL
                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Testis;
Nakamura Y., Inoue M., Okumura Y., Shiota M., Nishikawa M., Arase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ndmo saptaras, namenus.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                   "Cloning, expression analysis, and tissue distribution of esp
                                                                                                                                                                                                                     1/testisin, a membrane-type serine protease from the rat.";
J. Med. Invest. 50.78-86(2003).
Invest. Sol.78-86(2003).
EMBL; ABO74516; BAC57949.1;
HSSP; P00766; ICHG.
                                                                                                                                                                                                                                                                                                                          MERCES SOLUTIONS.

MERCES SOLUTIONS.

GO; GO: 0004263; F: chymotrypsin activity; IEA.

GO; GO: 0008233; F: peptidase activity; IEA.

GO; GO: 0006203; F: trypsin activity; IEA.

GO; GO: 0006203; F: proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

PROMITS; PR00122; CHYMOTRYPIN.

SMART; SM00020; Trypsin.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN INS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 AA; 36631 MW; 7F6C0B204802B963 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.3%; Score 1128.5; DB Best Local Similarity 63.5%; Pred. No. 2.4e-92; Matches 205; Conservative 40; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Protease; Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 MIRNGMLRPDPAPLLLFLTLAWA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAQSGMSQPDPSWPLLFFPLLWA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created 01-MAR-2004 (TrEMBLrel. 26, Last se 01-MAR-2004 (TrEMBLrel. 26, Last an Testis serine protease 1 precursor. Name=TESSP1; Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
        Rattus norvegicus (Rat)
                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7RTY9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7RTY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFWSLQAYYTRYFVSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFEN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIDCWVIGWGYIKEDEALPSPHILQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 RIDCWVIGWGAIGEDESLPSPNILOEVQVAIINNSMCNHMYKKPDFRINIMGDMVCAGTP 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 QGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGARGALILLALL--LARAGL------RKPESQEAAPLSGPCGRRVITSRIVGGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Gaps
                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI1916698; Pres21.

R GO; GO: GO05615; C: extracellular space; TAS.
GO; GO: GO005224; C: extracellular space; TAS.
R GO; GO: GO004225; F: serine-type endopeptidase activity; IDA.
R GO; GO: GO07233; P: spermatogenesis; TAS.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001314; Peptidase_S1.
R InterPro; IPR001314; Peptidase_S1.
R PRINTS; PR000723; CHYMOTRYPSIN.
R PRANT; SM00020; TYPP_SC; 1.
R PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
R PROSITE; PS00135; TRYPSIN HIS; INKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 1152; DB 2; Length 336; 65.0%; Pred. No. 1.9e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 336 AA; 37361 MW; E5206FEDBE55C670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07N-2004 (TrEMBLrel. 26, Last annotation update)
Eosinophil serine protease-1.
                                                                                                                                                    and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: Belongs to peptidase family SI
EMBL; BC049588; AAH49588.1; -.
HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 SGMSQPDPSWPLLFFPLLWALPLLGP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGLLRPDPVPLLLFLTLAWASSLLRP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase, Protease, Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 65.0%
Les 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
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유 ò 원 à 셤 ò 유 ò 셤 ò

237

SEPPRE

224

117

44 9

Gaps

19;

59; Indels

DB 2; Length 328;

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49 ELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 MQGRWPWQASLRLKKSHRCGGSLLSRRWVLTAAHCFRKY---LDPEKWTVQLGQLTSKPS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 FWSLQAYYTRYFVSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 TDCWVTGWGYIKED-EALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 QGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGIQGPVLLLLLLC-VMLGKPGSREESQAADLKSTDIKLLSMPCGRRNDTRSRIVGGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninici P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGARGALLLALLLARAGLRKPESQEAAP-----LSGPCGRRVIT-SRIVGGEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     099413;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4931440B09 product:TESTIS SERINE PROTEASE-1
                                                                                                                                                                                                                                                                                                                                                                                                    49.2%; Score 850; DB 2; Length 322; 52.8%; Pred. No. 1.7e-67; ive 43; Mismatches 93; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/61; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
         Matsui H., Takano N., Takahashi T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY; Balongs to peptidase family S1.
EMBL; AB049453; BBE68561.1; -.
HSSP; P00766; 1CHG.
                                                                                                                                                 MGD; MGI:1918253; 4931440B09Rik.

GO; GO:0005615; C:extracellular space; TAS.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN SER; 1.

Hydrolase; Perctease; Serine protease.
SEQUENCE 322 AA; 36218 MW; ED55F9A199A3B491 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 SGMSQPDPSWPLLFFPLLWALPLLGP 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 52.8%
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homolog.
Name=4931440B09Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 NRTDCWVTGWGYIK-EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 NAQGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLM 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 DAELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSM 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGARGALLLALLLARAGLRKPESQEAAPLSGP-------CGRRVITSRIVGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                          MEDLINE=22722134; PubMed=12838346;
Puente X.S., Sanchez L.M., Overall C.M., Lopez-Otin C.;
Puente X.S., Sanchez L.M., Overall C.M., Lopez-Otin C.;
Nat. Rev. Genet. 4:544-558(2003).
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Belongs to peptidase shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.0%; Score 881; DB 2; Length 318; 53.7%; Pred. No. 2.9e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Indels
                                                                                                                                                                                                                                                             MEROPS; SOLUZZ; ...
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PF00099; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN 21 318 testis serine protease 1. SEQUENCE 318 AA; 35078 MW; D792213630CF15C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
101-DR-2004 (TrEMBLrel. 26, Last annotation update)
Testis serine protease-1.
Name-4931440B09Rik; Synonyms-tessp-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase, Protease, Serine protease, Signal.
SIGNAL 1 20 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 AQSGMSQPDPSWPLLFFPLLWA 307
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                                                                                                                                                                                                                   EMBL; BN000124; CAD67575.1;
HSSP; P08709; 1FAK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 173;
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EX COC OR DET TO SERVICE SERVI

59 LDPEKWTVQLGQLTSKPSYWNRKAYSGRYRVKDIIVNSEDKLKS-HDLALLRLASSVTYN 117

2 PCGRRNDTRSRIVGGIESMQGRWPWQASLRLKKKSHRCGGSLLSRRWVLTAAHCFRKY--91 SDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRYLGNSPYDIALVKLSAPVTYT

210 KYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPG

151 KHIQPICLQASTFEFENRTDCWVTGWGYIKED-EALPSPHTLQEVQVAIINNSMCNHLFL

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28

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RESULT 8
Q6BEA2
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A Arakawa T., Bono H., Carminci P., Fukuda S., Fukuda Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojina Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yammura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
L. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
C -i - SIMILARITY: Belongs to peptidase family Sl.
R EMBL, AKO16509; BABS0277.1; -
                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazati Y., Muramateu M., Hayashizaki Y.; Nuramatization of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CSTBL/6J; TISSUE-Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunioto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Foreda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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PRINTS; PR00722; CHYMOTRYBSIN.
SMART; SMO0203; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS01334; TRYPSIN JES; UNKNOWN_1.
PROSITE; PS0135; TRYPSIN JES; UNKNOWN_1.
PROSITE; PS0135; TRYPSIN JES; UNCNOWN_1.
PROSITE; PS0135; TRYPSIN JES; 1.
PROSITE; PS0135; TRYPSIN JES; UNCNOWN_1.
PROSITE; PS0135; TRYPSIN JES; 1.
PROSITE; PS0135; TRYPSIN JES; 1.
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GO; GO:0005615; C:extracellular spac
InterPro; IPR001254; Peptidase_SI:
InterPro; IPR001314; Peptidase_SIA.
InterPro; IPR00903; Pept_Ser_Gys.
                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
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66 VCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQ----AYYTRYF 120
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121 VSNIYLSPRYLG-NSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYI 179
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SEQUENCE FROM N.A.

Adachi W., Norman B., Davis J., Piatigorsky J.;

T. "Comprehensive analysis of gene expression of rat corneal epithelium and limbal epithelium.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

I. SIMILARITY: Belongs to peptidase family S1.

R. EMBL, AB101677; BACG1507.1; -.

R. GO; GO:0004263; F:chymorrypsin activity; IEA.

R. GO; GO:0004263; F:crypsin activity; IEA.

R. GO; GO:0005269; F:rrypsin activity; IEA.

R. GO; GO:0005269; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001214; Peptidase_S1A.

R. InterPro; IPR00120314; Peptidase_S1A.

R. InterPro; IPR0010314; Peptidase_S1A.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                 270 VYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPLLGP 313
                                                                                                                   PEAM; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPF: 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS0134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS0135; TRYPSIN HIS; UNKNOWN 1.
HYDCOLAS; Protease; Serine protease.
SEQUENCE 328 AA; 35803 MW; 9235EECAP62C1358 CRC64;
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Last annotation update)
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PCGRRVIT-SRIVGGEDAELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHCFETYSDL

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10; 66 VCGVSLLISHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQ----AYYTRYF 120 121 VSNIYLSPRYLG-NSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYI 179 180 KEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFR----KDIFGDMVCAGNAQGGKDACF 235 8 ALLLDPLLLRSGL------PACGHPRMFNRWVGGDALEGEWPWQVSIQRNGAH 55 6 ALLLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWDSH 65 45; Gaps Query Match 34.6%; Score 597.5; DB 2; Length 321; Best Local Similarity 43.3%; Pred. No. 6.1e-45; Matches 136; Conservative 38; Mismatches 95; Indels 45; g 셤 셤 ò ઠ 8 8

223 GDSGGPLVCLVDQSWVQAGVISWGEGCARRNRPGVYIRVASHYQWIHQIIPELQPQGRAG 282 GDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLM-----AQ 287 321 AA. 288 SGMSQPDP-SW-PL 299 283 SQQQQRDPRGWQPL 296 STANDARD; HUMAN 236 8 셤

Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo. Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M., Wolters P.J., Verghese G.M.;

Wolters P.J., Verghese G.M.;

Characterization of human gamma-tryptases, novel members of the chromosome 16p mast cell tryptase and prostasin gene families.";

J. Immunol. 164:6566-6575(2000). Q9NNRZ1, Q9C015, Q9NRQ8; Q9UBB2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase) SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2) MEDLINE=20302813; PubMed=10843716; Name=TPSG1; Synonyms=TMT; Homo sapiens (Human) NCBI\_TaxID=9606; 

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mouse and SEQUENCE FROM N.A. MEDLINE=99452974; PubMed=10521469; DOI=10.1074/jbc.274.43.30784; MEDLINE=99452974; PubMed=10521469; DOI=10.1074/jbc.274.43.30784; Medline G., Tang Y., Feyfant B., Sali A., Li L., Li Y., Huang C., Friend D.S., Krilis S.A., Stevens R.L.; "Identification of a new member of the tryptase family of mouse a human mast cell proteases which possesses a novel COOH-terminal hydrophobic extension."; J. Biol. Chem. 274:30784-30793(1999). SEQUENCE OF 220-321 FROM N.A.

Mittman S., Agnew W.S.;
"Organization and alternative splicing of CACNAIH.";
Submitted (JAN-201) to the EMBL/GenBank/DDBJ databases.
-I. SUBCELLULAR LOCATION: Membrane-anchored (Potential).
-I. TISSUB SPRCIFICITY: Expressed in many tissues.
-I. POLYMORPHISM: There are two alleles; gamma-I and gamma-II which differ by 5 residues. subfamily.

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Genew, HGNC:14134; TPSG1. InterPro; IPR009003; Pept Ser\_Cys. InterPro; IPR001254; Peptidase\_S1. InterPro; IPR001314; Peptidase\_S1A. EMBL, AF191031, AAF76457.1; -.
EMBL, AF1795508; AAF76458.1; -.
EMBL, AF175752; AAF03697.1; -.
EMBL, AF775523, AAF03695.1; -.
EMBL, AF233563; AAG48852.2; -. Pfam; PF00089; Trypsin; MEROPS; S01.028;

PRINTS; PR00722; CHYMOTRYPSIN

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Name=tmprss9-prov;
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NCBI_TaxID=8364;
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                                NCBI_TaxID=9606;
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                                                                                     Tryptase gamma.

Tryptase gamma light chain.

Tryptase gamma heavy chain.

Potential.

Charge relay system (By similarity).

Charge relay system (By similarity).

Charge relay system (By similarity).

Interchain (Potential).

By similarity.

N-linked (GICNAC...) (Potential).
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
Glycoprotein; Hydrolase; Polymorphism; Serine protease; Signal; Transmembrane; Zymogen.
                                                                                                                                                                                                                                                                                                                                                DB 1; Length 321;
                                                                                                                                                                                                                                                                                                                                              Query Match 34.5%; Score 596.5; DB 1; Length Best Local Similarity 42.7%; Pred. No. 7.5e-45; Matches 138; Conservative 40; Mismatches 100; Indels
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FFF7B06E3C4A962D CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
HS transmembrane tryptase; gene name TWT; AF175522_1.
                                                                                                                                                                                                        N-linked (GlCNAc. .)
M -> V (in gamma-II).
/FTId=VAR 012097.
                                                                                                                                                                                                                                                                           -> I (in gamma-II).
FTId=VAR_012100.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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Homo sapiens (Human)
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56 RLRRVHVCGGSLLSPQWVLTAAAHCFSGSLNSSD---YQVHLGELEITLSPHFSTVRQII- 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 YIKEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFG------DMVCAGNAQG 229
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                                                                                                                                                                                                                 Higgs D.R.;

Higgs D.R.;

The short arm of human chromosome 16.";

The short arm of human chromosome 16.";

Thus, Mol. Genet. 10:339-352(2001).

Thum. Mol. Genet. 10:39-352(2001).

The short arm of human chromosome 16.";

Thum. Mol. Genet. 10:39-352(2001).

Thum. Mol. Genet. 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ALGACGLILILIAVPGV----SLRTLQPGCGRPQVSDAGGRIVGGHAAPAGAWPWQASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 RLWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQL--TSMPSFWSLQAYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ARGALLLAALLLARAGLRKPESQEAAPLSGPCGRRVIT---SRIVGGEDAELGRWPWQGSL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
SEGUENCE FROM N.A.
MEDLINE-21096910; DDMed=11157797; DOI=10.1093/hmg/10.4.339;
Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.5%; Score 595.5; DB 2; Length 321; 42.7%; Pred. No. 9.2e-45; tive 40; Mismatches 100; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS0134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease; Transmembrane.
SEQUENCE 321 AA; 33829 MW; FFF50895DC4FC73D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 GSESGYPRLPLLAGFFLPGLFLL 296
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Matches 138, Conservative
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55

213

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PRT;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Thymus;
                      (TrEMBLrel. 23,
PRELIMINARY;
                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium;
                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=10090;
                      01-MAR-2003
                                                                                       Name=Mpn;
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AHCFE---NSQFPSDYEVRLGTYRLAQTSPN----EITYTVDRIIVNSQFDSSTLFG--- 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 YDIALVKLSAPVTYTKHIQPICLQASTFEFFRRTDCWVTGWGYIKEDEALPSPHTLQEVQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 VAIINNSMCN---HLFLKYSFRKDIF-GDMVCAGNAQGGKDACFGDSGGPLACNKDGLWY 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 AHCPETYSDLSDPSGWMVQFGQ---LISMPSFWSLQAYYT--RYFVSNIYLSPRYLGNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Gaps
                                                                                                                                                                                                                                                                                     TISSUE-Whole body:

Klein S., Gerhard D.S.;
Klein S., Gerhard D.S.;
Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.

S. SIMILARITY: Belongs to peptidase family S1.

EMBL; BC075293; AAH75293.1; -.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR001254; Peptidase S1.

R InterPro; IPR001314; Peptidase S1A.

InterPro; IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.9%; Score 586; DB 2; Length 719; Best Local Similarity 43.3%; Pred. No. 1.6e-43; Matches 117; Conservative 43; Mismatches 90; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, Protease, Serine protease.
SEQUENCE 719 AA; 76098 MW; 906346A21D8834C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 QIGVVSWGVGCGRPNRPGVYTNISHHFEWI 281
                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0722; CHYMOTRYPSIN.
SMART; SMO020; Tryp SPC; 2.
PROSITE; PSS0240, TRYPSIN DOM; 2.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_2.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; Trypsin; 2
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
         PROM N.A
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RESULT Q8BJR6

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STRAIN=C5/BL/6J; TISSUE=Thywus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayabilzaki Y.; Highlizaki Y.; Highlizaki Y.; Highli-efficiency full-1ength cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                     01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
05-UIL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus 3 days neonate thymus chywus KIKEN full-length enriched
library, clone:A630023F11 product:similar to MARAPSIN (EC 3.4.21.-)
(Pancreasin) (Channel-activating protease 2-like protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunbata K., Itoh M., Alzawa K., Nagaoka S., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumioto H., Sakaguchi S., Ikegami T., Kashiiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watshiiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
328 AA.
                                                                                                 Created)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VSNIYLSPRYLG-NSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 KEDEALPSPHTLQEVQVAIINNSMCNHLF---LKYSFR-KDIFGDMVCAGNAQGGKDACF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 ALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94; Indels 28; Gaps
                                                                                                    "Structure and activity of human pancreasin, a novel tryptic serine peptidase expressed primarily by the pancreas."; J. Biol. Chem. 5:3363-3371(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 GDSGGPLVCLVDQSWVQAGVISWGEGCARRNRPGVYIRVTSHHKWIHQIIPE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
[7]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Bladder;
MEDLINE=22439795; PubMed=12441343; DOI=10.1074/jbc.M209353200;
                                                                      Clair J., Wolters P.J.,
                                                                                                                                                                                                  FNOTALES, Protease; Serine protease.

SEOUENCE 328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 33.9%; Score 585; DB 2; Local Similarity 44.2%; Pred. No. 8.1e-44; Nes 129; Conservative 41; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSS8 HUMAN STANDARD; PRT; 343 AA. Q16651; Q9UCA3; O1-NOV-1997 (Rel. 35, Created) 25-OCT-2004 (Rel. 35, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Prostasin precursor (EC 3.4.21.-).
                                                                      Bhagwandin V.J., Hau L.W., Mallen-St
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                           STRAIN=129/SvJ;
                                                                                        Caughey G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=PRSS8;
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 RARAR 
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Riansner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heibh F., Bratchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Reneration and initial analysis of more than 15,000 full-length human and mouse colla sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       its C-terminus.
-!- TISSUB SPECIFICITY: Found in prostate, liver, salivary gland, kidney, lung, pancreas, colon, bronchus and renal proximal tubular cells. In the prostate gland it may be synthesized in epithelial cells, secreted into the ducts, and excreted into the seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Membrane-bound. Secreted after cleavage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gland.";
J. Biol. Chem. 269:18843-18848(1994).
-!- FUNCTION: Possesses a trypsin-like cleavage specificity.
-!- SUBUNIT: Heterodimer of two chains, light and heavy, held by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu J.X., Chao L., Chao J.; "Prostasin is a novel human serine proteinase from seminal fluid. Purification, tissue distribution, and localization in prostate
                                                                                                                                      Yu J.X., Chao L., Chao J.;
"Molecular cloning, tissue-specific expression, and cellular
localization of human prostasin mRNA.";
J. Biol. Chem. 270:13483-13489(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 600823; -.
GO; GO:0005615; C:extracellular space; TAS.
FROM N.A., AND PARTIAL SEQUENCE
                                         TISSUE=Prostate;
MEDLINE=95286644; PubMed=7768952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94308140; PubMed=8034638;
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EMBL; U33446; AAB19071.1; -.
EMBL; BC001462; AAH01462.1; -.
PIR; A57014; A57014
HSSP; P00760; 1EZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.159; -.
Genew; HGNC:9491; PRSS8.
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MIM; 600823; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 45-64.
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 YFVSNIYLSPRYL-GNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWG 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 YIKEDEALPSPHTLQEVQVAIINNSMCNHLF---LKYSFRKDIFGDMVCAGNAQGGKDAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 HVAPSVSLLTPKPLÓQLEVPLÍSRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGKDAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 FGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQ-----KLMA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 <u>Q</u>ĠĎŚĠĠPĹSĊPVEĠĹŴŸĹŢĠĬVŚŴĠĎAĊĠARŇŘPĠVŸŤĽAŚSYASŴĬQSKVŢELQPRVVP 294
                                                      R InterPro; IRR001314; Peptidase_SIA.

R Pfam; PR00089; Trypsin; 1.

R PRINTS; PR000220; Trypsin; 1.

R RNART; SM00020; Tryp SPC; 1.

R PROSITE; PS00140; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease; SiGNAL 1 29 Prostation peptide.

T SIGNAL 1 29 Prostasin light chain.

T CHAIN 45 32 Prostasin light chain.

T TRANSNEM 320 343 Potential.

T DOMAIN 45 286 Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 VCGGSLVSEQWVLSAAHCF-----PSEHHKEAYEVKLGAHQLDS----YSEDAKVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 ALLILALILLARAGIRKPESQEAAPISGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ALLIXIGILRSG-TGAEGAEA----PCG-VAPQARITGGSSAVAGOWPWOVSITYBGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                               -linked (GlcNAc. . .) (Potential) 98DD6447F5A8C1B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 579.5; DB 1; Length 343; 41.0%; Pred. No. 2.7e-43; tive 45; Mismatches 101; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 QSGMSQPDPSW-------PLLFFPLLWALPLLGP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: |||| :
QTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALGLLSP 338
                                                                                                                                                                                                                                                                            Serine protease.
Interchain (By similarity).
By similarity.
By similarity.
By similarity.
Charge relay system.
Charge relay system.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
InterPro; IPR001031, Peptidase Cys.
InterPro; IPR001254; Peptidase Si.
InterPro; IPR001314; Peptidase Si.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               N-linked
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epidermis specific serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                             36431 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             343 AA;
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ACT_SITE
CARBOHYD
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89 -----DLSDPSGWMVQFG--QLTSMPSFWSLQAYYTRYFVSNIYLSPRYLGNSPYDIA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 NNSMCNHLFLK-----YSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKDGLMYQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 DSSVCGTMYESSLGYIPDFSFIQE---DMVCAGYKEGRIDACQGDSGGPLVCNVNNVWLQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 IGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPLLG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 TVYLGAYQLSAPDNSTVSRGVKSITKHPDF--------QYEGSSG-DIA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 LGIVSWGYGCAEPNRPGVYTKVQYYQDWLKTNVPLIVFSEEGPS------VAPSIG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 CGRRVITSRIVGGEDABLGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHCFETYS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Indels
                            Yamada K.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-i- SINTLARITY: Belongs to peptidase family S1.
EMBL, ABO1869; BAA84941.1; -
HSSP; P00760; 1EZX.
                                                                                                                                                                                     Hast; EUU,00; ILEA.

GO; GO:0004253; F:chymotrypsin activity; IEA.

GO; GO:0004253; F:trypsin activity; IEA.

GO; GO:0004255; F:trypsin activity; IEA.

GO; GO:0004255; F:trypsin activity; IEA.

GO; GO:0004268; P:trypsin activity; IEA.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR001314; Peptidase_S1A.

INTERPO; PRO0009; Trypsin; 1.

PRINTS; PR00125; CHYMOTRYPSIN.

SWART; SM00020; Tryp_SPC; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

HYdrolase; Protesse; Serine protesse.

SEQUENCE 389 AA; 42375 MW; B31FB4A2F5D1F6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42375 MW; B31FB4A2F5D1F6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 575.5; DB 2;
39.9%; Pred. No. 6.9e-43;
tive 44; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: February 27, 2005, 20:18:32
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241 CTGGGCACTCACGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300
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AR410808 Sequence
AR439172 Sequence
AR473192 Sequence
AR57178 Sequence
AR56711 Sequence
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AR56714 Sequence
AR567314 Sequence
BD075578 Secretory
AY359034 Homo aapi
AR253955 Sequence
E21866 Novel acido
E21867 Novel acido
AX370459 Sequence
AX370459 Sequence
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BD172438 Sedreted
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AR253955
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AB031329
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Maximum DB seq length: 200000000
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FT source /organism='Homo sapiens (human)'.
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                                               Patent: JP 2002223786-A 211 13-AUG-2002;
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18-DEC-2001 JP 2001385135
17-SEP-1997 US 60/0591:
                                                                            Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA
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                                                                                              CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC
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Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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JP 2002223786-A/211.
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(C12NS/00,C12R1:31)
(C12NS/10,C12R1:61)
(C12NS/10,C
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/organism='Homo sapiens (human)'
Location/Qualifiers
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                                                                                   Yuan, J.
Secreted and transmembrane polypeptides and
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Pred. No. 1.5e-264;
0; Mismatches 4;
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                                                                                                                                                        Patent: JP 2002238586-A 211 27-AUG-2002,
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                      JP 2001385205
US 60/0591
                                                                                                                                                                                     GENENTECH INC
OS Homo sapiens (human)
PN JP 2002238586-A/211
PD 27-AUG-2002
PF 18-DEC-2001 JP 200138:
PR 17-SEP-1997 US 60/6
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Best Local Similarity 99.6
Matches 1093; Conservative
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17-SEP-1997 US
18-SEP-1997 US
18-SEP-1997 US
21-OCT-1997 US
24-OCT-1997 US
22-OCT-1997 US
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AUTHORS
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JP 2002238586-A/211.
Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                               CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC
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                                                                                                                                    GTGGATGGTCCAGTTTGGCCAGCTGCTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA
                                                                                                                                                                                                                                               CTACACCCGTTACTTCGTATCGAATATCTTGAGCCCTCGCTACCTGGGGAATTCACC
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BD172757
LOCUS
DEFINITION
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PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC C12N15/02,

PC C12N15/02,

C12P21/02,C12P21/08/(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC (C12P21/02,C12R1:645),C12N15/00,C12N15/00,C12N15/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the
                                                                                                                                                             nucleic acids encoding
                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1100)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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    1100
/organism='Homo sapiens (human)'.

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GENENTECH INC

S Home appiens (human)

PD 2002238587-A/211

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385248

I7-SEP-1997 US 60/059115,17-SEP-1997 US 17-SEP-1997 US 60/059115,17-SEP-1997 US 17-SEP-1997 US 60/059113,17-SEP-1997 US 17-SEP-1997 US 60/059113,17-SEP-1997 US 21-OCT-1997 US 60/053120,24-OCT-1997 US 24-OCT-1997 US 60/053120,24-OCT-1997 US 60/053120,24-OCT-1997 US 24-OCT-1997 US 60/053120,24-OCT-1997 US 60/053120,24-OCT-1997 US 28-OCT-1997 US 60/053120,24-OCT-1997 US 28-OCT-1997 US 60/053120,24-OCT-1997 US 28-OCT-1997 US 60/053120,24-OCT-1997 US 29-OCT-1997 US 60/053120,24-OCT-1997 US 29-OCT-1997 US 60/053120,21-OCY-1997 US 60/053120,21-OCY-1997 US 60/053120,21-NOV-1997 US 60/055120,21-NOV-1997 US 24-NOV-1997 US 60/055120,21-NOV-1997 US 60/055120,21-NOV-1997 US 24-NOV-1997 US 60/055120,21-NOV-1997 US 24-NOV-1997 US 60/055120,21-NOV-1997 U
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Pred. No. 1.5e-264;
0; Mismatches 4;
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/organism="Homo sapiens"
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64 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCTTATCAGGACCATGCGGCCG

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12.1   ACCOSTICACION CONTENTION PROGRAMMENT	TION Secreted and transmembrane polypeptides and nucleic ac the same.  No. B173395.  No. B173395.  No. B173395.  No. B173395.  No. B173395.  Homo sapiens (human)  NISM Homo sapiens (human)  NOES Wood, W. I., Gutney, A. L., Goddard, A., Pennica, D., Zheng, Yuan, J.  Secreted and transmembrane polypeptides and nucleic ac the same  NAB. Patent: JP 2002238588-A/211  R. D. 2002238588-A/211  P. D. 2002238588-A/211  No. Homo sapiens (human)  P. D. 2002238588-A/211  P. D. 200223858-A/211  P. SEP-1997 US  60/0639113,17-SEP-1997 US  60/063912  24-0CT-1997 US  60/063912,10-CT-1997 US  60/063912  24-0CT-1997 US  60/063940,12-0CT-1997 US  60/	24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840  WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNU JIAN ZHENG, PL CIZNIS/09, CO7KL4/435, CO7KL6/18, CO7KL3/00, CIZNIJ/19, C CIZNIS/10, PC CIZNIS/10, CIZRI:91), CIZNIJ/19, CIZRI:645), (CIZNIJ/21) PC (CIZNIJ/20, CIZRI:91), CIZNIJ/19, CIZRI:645), (CIZNIJ/21) PC (CIZNIJ/20, CIZRI:91), CIZNIJ/19, CIZRI:645), (CIZNIJ/21) PC (CIZNIJ/20, CIZRI:91), CIZNIJ/19, CIZRI:645), (CIZNIJ/21) RE KRY FT KRY PT Location/Qualifiers I . 1100  Organism="Homo sapiens"    Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"   Organism="Homo sapiens"
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	ACGGGTCATCACGTCGCGCATCGTGGGTGGAGACGCCGAACTCGGGGCTTGGCCGTG  ACGGGTCATCACGTCGCGCATCGTGGGTGGAGACGCCGAACTCGGGCGTTGGCCGTG  ACGGGTCATCACGTCGCGCATCGTGGGTTGGGGACCCGAACTCGGGCCTTGGCCCC  GCGGGGGGGGGCCTGGTGGGTTCCCACGTATGCGGATGACCTGGTCCCCC  GCAGGGGGGCCTGCTGGGATTCCCACGTATGCGGATGACCTGCTCAGCCCCC  GTGGGCACTCACGGCGCCTGTGGGATTCCCACGTATGCGAGCCTGCTCCCCCC  CTGGGCACTCACGGCGCCACTGTGTTTGAACCTTTTGTTGTTTTTTTT	CGTGAGCTGGGGAGTGGGTCGGCCCAATCGGCCCGGTGTTCTACACCAATATCAG 840  CGTGAGCTGGGGAGTGGGTCGGCCCAATCGGCCCGGTGTTCTACACCAATATCAG 843  CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAGTGTTCTACACCAGACACC 900  CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAGAGTGGCATGTCCCAGCCAG

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Homo sapiens (human)
JP 2002253280-A/211
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C12P21/08, (C12N1/19,C12R1:645), (C12N1/21,C12R1:19), (C12N5/10,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1100)
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2 AG1P25/16,AG1P25/28,AG1P31/12,AG1P35/00,C07K14/47,C07K16/18,

2 C07K19/00,

C12N1/19,C12N1/21,C12N5/10//AG1K38/00,AG1K39/395,AG1K39/395,
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C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06,
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Yuan,J.
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1. .1100
/organism='Homo sapiens (human)'
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Pred. No. 1.5e-264;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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17-SEP-1997 US 60/0591:
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Best Local Similarity
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Unclassified.

1 (bases 1 to 1100)
Ashkenazi,A., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
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99.1%; Score 1090.6; DB 6
Best Local Similarity 99.6%; Pred. No. 1.5e-264;
Matches 1093; Conservative 0; Mismatches 4;
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Location/Qualifiers
1. 1100
/organism="unknown"
/mol_type="genomic DNA"
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Seguence 256 from patent US 6635468.
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   CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCA
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LOCUS LOCUS LOCUS Sequence 256 from patent US 6686451.  DEFINITION Sequence 256 from patent US 6686451.  ARAT3192 ARAT3119 ARAT3119 ARAT3119 ARAT3110 ARAT31	Query Match         99.1%;         Score 1090.6;         DB 6;         Length 1100;           Best Local Similarity         99.6%;         Pred. No. 1.5e-264;         Accession of the conservative of the conservation of the conservati	Oy         61 GGCTGGACTCAGGAAGTCGCAGGAGGCGCGCGTTATCAGGACCATGCGGCCG 120           Db         64 GGCTGGACTCAGGAAGTCGCAGGAGGCGCCGTTATCAGGACCATGCGGCCG 123           Qy         121 ACGGGTCATCACGTCGCAGTCGGGTGAGAGGCCGCATACTCGGGCGTTGGCCGTG 180           Db         124 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTG 183           Qy         181	184   GCAGGGAACCTGCTGCTGTATCCCACCTATGCGATCAGCCTGCTCAGCCAGC	QY         421 CTATGACATTGCCTTGGTGAGCTGTCACCTACACTAAACACTTCCAGCC 480           DD         424 CTATGACATTGCTTGAGACTGTCACCTGCACCTCAAACACATCCAGCC 483           QY         481 CATCTCTCCAGGCCTCCACATTTGAGTTTGAGACCGGACGACTGCTGGTGACTGCTGGTGACTGCTGGTGACTGCTGGTGACTGCTGGTGACTGCTGAGTACTGCTGAGACTGCTGAGATCTGCTGAGACTGCTGAGATCTGCTGAGACTGCTGAGATCTGCTGAGACTGCTGAGATCTGCTGAGAACTCAGAACTACAGAACTCAGAACTACAGAACTACAAAAAAAA

AUTHORS	JOURNAL	FEATURES	ORIGIN	Query Mate Best Loca	Matches ]	S	3 8	qq	0%	qa	δ	qa	λ̈σ	qa	δ	đ	ð	q <sub>Q</sub>	λ̈σ	q <sub>Q</sub>	à	qa	ò	qq	ò	ДD	γ	qa	č	qa	λδ	qa	ò
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Unknown. Unclassified. 1 (bases 1 to 1100)

REFERENCE

Oy 361 CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC	Qy 421 CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAACACATCCAGCC	Qy 481 CATCTGTCTCCAGGCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG	Qy 541 CTGGGGGTACATCAAAGGGATGAGGCACTGCCGACCCCCCACACCTCCAGGAAGTTCA	OY 601 GGTCGCCATCATAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA	QY         661         GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGAGGAAGGA	OY 721 CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGT	Qy 781 CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACAATATCAG	Qy 841 CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAGAGTGGCATGTCCCAGCCGAGCCG 	Oy 901 CTCCTGGCGCTACTCTTTTTCCCTCTTGGGGTCTCCCCACTCCTGGGGCCGGTCTG	Qy 961 AGCCTACCTGAGCCCATGCAGCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTG	Qy 1021 TCTTGTTTGGTAATAACACATTCCAGTTGATGCCTTGCAGGCATTTTTCAAAAAAAA	Oy 1081 AAAAAAAAAAAA 1097 		NA Secretory and transmembrane polypeptide and nucleic the same. 1 BD075578.1 GI:22621181	KEYWORDS JP 2001516580-A/211. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	Mammalia; Eucheria; Primates; Catarrinii; Hominidae; Homo. REFERENCE 1 (bases 1 to 1100) AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J. TITLE Secretory and transmembrane polypeptide and nucleic acid encoding	the same
901 CTCCTGGCCGCTACTTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG 960	961 AGCCTACCTGAGCCCATGCAGCCTGGCGAGTCAGGCCTGGTTCTTCTG 1020	1021 TCTTGTTTGGTAATAAACACATTCCAGTTGATGCCTTGCAGGGCATTTTTCAAAAAAAA	1081 AAAAAAAAAAAAA 1097 		AX697665 From Patent WO0104311. AX697665 A Grow Patent WO0104311. AX697665 AX697665.1 GI:29498754	Homo sapiens Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	Mammalla; Eucherla; Frimates; Catarrhin; Hominidae; Homo. Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,	Goddard, A., Goddowski, P.J., Giimaldi, C.J., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.P., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding	tne same Patent: Wo 0104311-A 256 18-JAN-2001; Genentech Inc. (US) Location/Qualifiers	1itomo sapiens" /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	<pre>y Match y match y match be some 1090.6; DB 6; Length 1100; local Similarity 99.6%; Pred. No. 1.5e-264; hes 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</pre>		61         GGCTGGACTCAGGAGGCGGCGGCGGCGTTATCAGGACCATGCGGCG         120           64         GGCTGGACTCAGGAGGCGGCGGCGTTATCAGGACCATGCGGCCG         123	121 ACGGGTCATCACGTCGCGCATCGTGGGTGGGGGGCGCGAACTCGGGCGTTGGCCGTG	181 GCAGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG 240	241 CTGGGCACTCACGGGGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300 244 CTGGGCACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCTCCGG 303	101 でかならないたいかんないであるのでですのできないできないできないできないできないのできないのできない。

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/organism='Homo sapiens (human)'
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1100 bp mRNA linear PRI 03-OCT-2003 Homo sapiens clone DNA42551 PRSS21 (UNQ266) mRNA, complete cds. AY359034 PLI CDNA Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1100). 1 (Dases 1 to 1100). Clark, H.F. Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Poster, J., Grimaldi, C., Gu, O., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,

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tive 0; Mismatches 0;
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Patent: US 6479274-A 3 12-NOV-2002;
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Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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                                      ACGGGTCATCACGTCGCGCATCGTGGAGAGGACGCCGAACTCGGGCGTTGGCCCGTG
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein séarch, using sw model

February 27, 2005, 20:11:50 ; Search time 25.5815 Seconds (without alignments) 1181.014 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-040-647-6 1728 1 MGARGALLLALLLARAGLRK.....PSWPLLFFPLLWALPLLGPV 314

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description			masc cerr crypcase plasma kallikrein	tryptase (EC 3.4.2	_	~	allikr	tryptase (EC 3.4.2	tryptase (EC 3.4.2	tryptase (EC 3.4.2	allikr	tryptase (EC 3.4.2	tryptase (EC 3.4.2	ion f	hepsin (EC 3.4.21.		acrosin (EC 3.4.21	_	plasmin (EC 3.4.21	membrane-bound arg	plasmin (EC 3.4.21	tryptase (EC 3.4.2	EC 3.4	apoprotein(a) (EC	low-density lipopr	enteropeptidase (E	acrosin (EC 3.4.21	testicular serine	enteropeptidase (E
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SUMMARIES	XE7014	A27014	KOMSPL	C35863	A38654	A35863	KORTPL	A47246	B35863	A32410	КОНИР	JC4171	A45754	KFHU1	S00845	JE0105	A34170	JX0172	PLHU .	JC7731	A61545	S68702	833777	800657	JE0315	A43090	829599	JE0104	A56318
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B61545	A47547	B30848	A37344	PLMS	PLPG	S11674	PLBO	S47538	S18407	S54146	146260	A32869	T30337	JC5759	B32410
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436.5	435	43	434	43				4	4	4					

## ALIGNMENTS

	RESULT 1
	AS7014 prostasin (EC 3.4.21) precursor - human
	C;Species: Homo sapiens [man)
	C.bace: 24-may-1550 #sequence_revision 24-may-1996 #text_cnange 05-Jui-2004 C.Accession: A57014; A54866
	R; Yu, J.X.; Chao, L.; Chao, J.
	o. blot. cuema: 2/v, 13+03-13+05, 1593 A. Title: Molecular cloning, tissue-specific expression, and cellular localization of hume
	A; Reference number: A57014; MUID: 95286644; PMID: 7768952
	A/Status: translated from GB/EMBL/DDBJ
	A; Molecule type: mRNA A Residues: 1-343 / RES
•	A;Cross-references: UNIPROT:Q16651; GB:L41351; NID:g862304; PIDN:AAC41759.1; PID:g862305
	A Experimental gource: prograte
	A;Note: parts or this sequence were determined by protein sequencing R:Yu. J.X.: Chao. L.: Chao. J.
	J. Biol. Chem. 269, 18843-18848, 1994
	A Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification, t
	A; Aregerence number: A54866; MU1D:94308140; PM1D:8034638 A: Aregerion: A54866
	A.Molecule twoe: profein
	A; Residues: 45-64 < VUA>
	C; Genetics:
	A,Gene: GDB:PRSS8
	A, Cross-references; GDB-57646; OMIM: 600823
	A; Map posttion: 10pli: 2-10pli: 2-
	C.Souberlaminis Liybein i Ciybein unduciogy C.Sowords : alvonorotein: hvdrolage: serine proteinase: transmembrane protein
	Fil-32/Domain: signal sequence #status predicted 651G>
	F;33-44,45-343/Product: prostasin #status predicted <mat></mat>
	F;33-44/Domain: prostasin light chain #status predicted <chl></chl>
	F:45-343/Domain: prostasin heavy chain #status predicted <chh></chh>
	F:323-431/Domain: transmembrane Hararus nredicted «TWMI»
	F;37-154,70-86,168-244,201-223,334-262/Disulfide bonds: #status predicted
	F. 185, 134, 238 Active site: Wis, Asp, Sor Heatus predicted
	FIFD9/Billioning Birde: carbonydrade (ABH) (COVALENC) #8darus GADELINGHGAL
	Query Match 33.5%; Score 579.5; DB 1; Length 343;
	Matches 141; Conservative 45; Mismatches 101; Indels 57; Gaps 12;
	QY 6 ALLLALLLARAGIRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWDSH 65
	:
	QY 66 VCGVSLLSHRWALTAAHCPETYSDLSDPSGWMVQPGQLTSMPSFWSLQAYYTR 118
	Db 69 VCGGSLVSEQWYLSAAHCFPSEHHKEAYEVKLGAHQLDSYSEDAKVST 116
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A; Molecule type: mRNA
A; Residues: 9-275 < VAN>
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A,Molecule type: DNA
A,Residues: 1-9 <VA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:PS0342; EMBL:D31789; NID:g517122; PIDN:BAA06598.1; PID:g5171
C;Superfamily: trypsin; trypsin homology
F;26-262/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S56160
R;Murakumo, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.;
Biochem. J. 309, 921-926, 1995
A;Title: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones A;Reference number: S56160; MUID:95366971; PMID:7639711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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                          235 FGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQ-----KLMA 286
                                                                                                                                                                                                           235 QGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKVTELQPRVVP 294
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YFVSNIYLSPRYL-GNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFFENRTDCWVTGWG 177
                                                                                       178 YIKEDEALPSPHTLQEVQVAIINNSMCNHLF---LKYSFRKDIFGDMVCAGNAQGGKDAC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                mast cell tryptase precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR----LW
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                                                                                                                                                                                                                                                                        287. QSGMSQPDPSW------PLLFFPLLWALPLLGP 313
                                                                                                                                                                                                                                                                                                                   <u><b>QTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALGLLSP 338</u>
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Matches 117; Conservative
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A;Cross-references: UNIPROT:P26262; GB:M58588; NID:g200359, PIDN:AAA63393.1; PID:g200359
A;Note: part of this sequence, including the amino ends of both the heavy and light chair C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex will c;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a lig are linked by one or more disulfide bonds.
C;Compent: The zymogen is activated by factor XIIa, which cleaves the molecule into a lig c;Cyberfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; filtrinolysis; glycoprotein; hydrolase; inflan F;10-199/Domain: apple repeat cAP1>
F;20-109/Domain: apple repeat cAP2>
F;20-109/Domain: apple repeat cAP2>
F;20-289/Domain: apple repeat cAP4>
F;21-380/Domain: apple repeat cAP4>
F;21-380/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
A;Note: the first nine residues of this sequence are inferred from genomic DNA of tryptas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptese (EC 3.4.21.59) III precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Paccession: Peb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Mar-2003
C;Accession: C35663; E35863; A38893
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.P. Proc. (Natl. Acad. Sa. R.), 311-31815, 1990
Proc. (Natl. Acad. Sa. R.), 311-31815, 1990
A;Fitle: Human mast call tryptase: multiple cDNAs and genes reveal a multigene serine proc. A;Reference number: A35863; MUID:90251647; PMID:2187193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 INARIVGGTNASLGEWPWQVSLQVKLVSQTHLCGGSIIGRQWVLTAAHCFDGIPYPDVWR 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 PSGWMVQFGQLT-SMPSFWSLQAYYTRYFVSNIYLSPRY-LGNSPYDIALVKLSAPVTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 YSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 ITSRIVGGEDAELGRWPWQGSLR---LWDSHVCGVSLLSHRWALTAAHCFE--TYSDLSD
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A;Cross-references: GB:M33493; NID:g339984; PIDN:AAA36780.1; PID:g339985
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21,Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
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; Pred. No. 5e-38;
42; Mismatches 85; Indels 23
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A;Reference number: A38893
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Matches 101; Conservative
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611 YTKVSEYMDWI 621
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A, Residues: 1-276 <REY>
A, Cross-references: UNTRROT: P21845; GB.MS7625; NID: G200506; PIDN: AAA39987.1; PID: G200507
A,Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37 as Gly, GAG for residue 168 as Gly for Resi
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A; Residues: 1-276 <RE2.>
A; Residues: 1-276 <RE2.>
A; Cross-references: GB: M57626; NID: g200508; PIDN: AAA39988.1; PID: g200509
R; Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-2234, 1990
A; Title: Different mouse mast cell populations express various combinations of at least
A; Reference number: A35646; MUID: 90222202; PMID: 2326280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 32-54 <RE3>
K; Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson,
Scand. J. Immunol. 38, 359-367, 1993
A; Hitle: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and
A; Reference number: 159478; MUID: 94023807; PMID: 8210998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Peb-1992 Hesquence revision 17-Peb-1994 #text_change 09-Jul-2004
C;Accession: A38654; B38654; D35646; I59478
R;Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991
A;Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by I
A;Reference number: A38654; MUID:91139682; PMID:1995638
                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 --SHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWNVQFGQLTSMPSFWSLQAYYTRYF- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 PVSRIIVHPQPYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 -VSNIYLSPR-YLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 IKEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKD----IFGDMVCAGNAQGGKDAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LILALPULASRA------YAAPAPGQALQRV---GIVGGQEAPRSKWPWQVSLRVRDR 53
                                                                                                                                                                                                                                                                                                                                                                                        7 LLLAL--LLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWD-
                                                                                                                                                                                                                                                                                                    36; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 QGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWI 267
                                                                                                                                                                                                      29.7%; Score 513; DB 2; Length 275; 40.1%; Pred. No. 2e-38;
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:22-31/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase I #status predicted <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted
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Superfamily: trypsin; trypsin homology
Keywords: hydrolase; serine proteinase; zymogen
                                                                                                                                                                                                                                                                                          43; Mismatches
                                                                                                                                                                                                                                                  Best Local Similarity ....
Matches 115; Conservative
                                                                                                                                                                                                                                             Local Similarity
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-0ct-1990 #sequence_revision 12-0ct-1990 #text_change 09-Jul-2004
C;Dates: 12-0ct-1990 #sequence_revision 13-0ct-1990 #text_change 09-Jul-2004
C;Accession: A35863; D35863; A60939; A39326
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.F.
Proc. Natl. Acad. Sci. US.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDMAs and genes reveal a multigene serine proc. A3;Reference number: A35863; MUID:90251647; PMID:2187193
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A; Residues: 31-38,'P', 40-41,'X', 43,'T', 45-48,'X',50 <BUT>
A; Experimental source: mast cell
A; Note: 44-G1y was also found
R; Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chretien, J.B.O., Chret. 262, 1363-1373, 1387
J. Balol. Chem. 262, 1363-1373, 1387
A; Title: Human pituitary tryptase: molecular forms, NH-2-terminal sequence, immunocytocht A; Reference number: A39326; MUID: 87109258; PMID: 3543004
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                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 --IKSPQLFRVQ------LREQYLYYGDQLLSLNRIVVHPHYYTAEGGADVALL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRY----FVSNIYLSPR-YLGNSPYDIALV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 KLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALPSPHTLQEVQVAIINN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMCNHLFLKYSFRKDIF----GDMVCAGNAQGGKDACFGDSGGPLACNKDGLWYQIGVVS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 PANQRV---GIVGGHEASESKWPWQVSLRFKLNYW-IHFCGGSLIHPQWVLTAAHCVGPH 80
                                                                                                                                                                                                                                                                                    PCGRRVITSRIVGGEDAELGRWPWQGSLRL----WDSHVCGVSLLSHRWALTAAHCFETY
                                                                                                                                                                                                     Gaps
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A; Residues: 1-275 < WB33491
A; Cross-references: GB:M33491
R; Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, P.C.
J. Leukoc. Biol. 47, 409-419, 1990
A; Title: Purification of tryptage from a human mast cell line.
A; Reference number: A60939; MUID:90244210; PMID:2110591
                                                                                                                                                                                                     34;
                                                                                                                       DB 2; Length 276;
                                                                                                                                                                                                 88; Indels
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C[Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase I #status experimental <MAT>
F;32-268/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted
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F;74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                   Query Match 29.6%; Score 511; DB 2; Best Local Similarity 39.3%; Pred. No. 3e-38; Matches 106; Conservative 42; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 WGVGCGRPNRPGVYTNISHHFEWIQKLMAQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tryptase (EC 3.4.21.59) I precursor - human
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A;Experimental source: pituitary
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A; Residues: 1-275 < VAN>
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                                                                                                                                                                                                                                                                                    32
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duplication; fibrinolysis; glycoprotein; hydrolase; inflan

8 유 à 셤 ò a à

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F;1-19/Domain: signal sequence #status predicted <81G>
F;20-390/Product: plasma kallikrein heavy chain #status experimental
F;20-109/Domain: apple repeat <API>
   C; Keywords: blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-273 <MCN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A47246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P14272; GB:J05315
A;Note: the authors translated the codon GAG for residue 81 as Gln
R;Seidah; N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, F.; Lazur
DNA 8, 563-574, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S06851
A;Molecule type: protein
A;Residues: 20-45;391-413 <PAQ>
R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, R.; Lazux
DNA Cell Biol. 8, 563-574, 1989
A;Title: The cDNA structure of rat plasma kallikrein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M30282; NID:g205010; PIDN:AAA41463.1; PID:g205011
A;Note: part of this sequence, including the amino ends of both the heavy and light chai
R;Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, N.G.
Biochim. Biophys. Acta 999, 103-110, 1989
A;Title: Rat plasma kallikrein: purification, NH(2)-terminal sequencing and development
A;Reference number: S06851; MUID:90089457; PMID:2597701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasma kallikrein (EC 3.4.21.34) precursor - rat
N;Alternate names: Fletcher factor; kininogenin; serum kallikrein
N;Alternate names: Fletcher factor; kininogenin; serum kallikrein
C;Species: Ratius norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A39180; A33320; S06851; I53041; S06852
B;Beaubien, G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay, M.; Chretien, M.; Seidah, N.G
Biochemistry 30, 1628-1635, 1991
A;Title: Gene structure and chromosomal localization of plasma kallikrein.
A;Reference number: A39180; MUID:91129236; PMID:1993180
                                                                  11;
                                                                                                                                                                                                                                                          -WDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
                                                                                                                                                                                                                                                                                                      54 YW-MHFCGGSLIHPQWVLTAAHC--VGPDVKDLAALRVQLRE------QHLYYQDQL 101
                                                                                                                                                                                                                                                                                                                                                                                      --VSNIYLSPR-YLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 YIKEDEALPSPHTLQEVQVALINNSMCNHLFLKYSFRKD----IFGDMVCAGNAQGGKDA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
                                                                                                                                  61
                                                                                                                                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                              162 DVDNDERLPPPFPLKOVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTR--RDS
                                                                                                                              7 LILLAL -- LLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRL ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWI 281
   Length 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: The cDNA structure of rat plasma kallikrein.
A,Reference number: A33320; MUID:90091743; PMID:2598771
29.5%; Score 510; DB 2; 39.9%; Pred. No. 3.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: not compared with conceptual translation
                                                               43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translated from GB/EMBL/DDBJ
                                 Best Local Similarity 39,9
Matches 115, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: I53041
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A; Residues: 1-638 <SEI>
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A;Residues: 1-638 <BEA>
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                                                                                                                                                                                                                                                                                                                                                                                         121
Query Match
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Fill0-199/Domain: apple repeat <AP2>
Fi20-289/Domain: apple repeat <AP3>
Fi20-280/Domain: apple repeat <AP3>
Fi20-280/Domain: apple repeat <AP4>
Fi391-6380/Domain: apple repeat <AP4>
Fi391-6380/Domain: typsin homology <TRX>
Fi391-621/Domain: trypsin homology <TRX>
Fi391-621/Domain: trypsin homology <TRX>
Fi21-104,47-77,51-57,111-194,1137,166,141-147,201-284,227-256,231-237,292-375,318-347,322-87127,215,308,453,459,494/Binding site: carbohydrate (Asn) (covalent) #status predicted Fi396/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q02844; GB:L00653; NID:g200518; PIDN:AAA39992.1; PID:g200519
A;Note: sequence extracted from NCB1 backbone (NCBIN:119745, NCBIP:119746)
C;Superfamily: trypsin homology
C;Superfamily: trypsin homology
C;Keywords: hydrolaes; serine proteinase
F;29-265/Domain: trypsin homology <TRX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 -TYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRY-LGNSPYDIALVKL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 SAPVIYIKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALPSPHTLQEVQVAIINNSM 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 CQXKYRDYVITK---QMICAGYKEGGIDACKGDSGGPLVCKHSGRWQLVGITSWGEGCA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 QTPLNYTEFQKPICLPSKADTNTIYTNCWVTGWGYTKERG--ETQNILQKATIPLVPNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tryptase (EC 3.4.21.59) 2 - mouse
C,Species: Mus musculus (house mouse)
C,Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 SSDCTTK-INARIVGGTNSSLGEWPWQVSLQVKLVSQNHMCGGSIIGRQWILTAAHCFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 CFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF----VSNIYLSPR-YLGNSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNHLFLKYSFRKD1FGDMVCAGNAQGGKDACFGDSGGPLACNKDGLWYQ1GVVSWGVGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AAP--GPAMTR---EGIVGGQEAHGNKWPWQVSLRANDTYWMFFCGGSLIHPQWVLTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 AAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWDS---HVCGVSLLSHRWALTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 SGPCGRRVITSRIVGGEDAELGRWPWQGSLR---LWDSHVCGVSLLSHRWALTAAHCFE-
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Gaps
                                                                                                                                                                                                                                                                                     29.5%; Score 510; DB 1; Length 638; 37.7%; Pred. No. 1e-37; tive 47; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86; Indels
                                                                                                                                                                                                                                   F;434,483,578/Active site: His, Asp, Ser #status predicted
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Pred. No. 4.5e-38;
                                                                                                                                                                                                                                                                                                                                                 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :||||| :: ::|| :: |
604 RKEQPGVYTKVAEYIDWILEKIQSS 628
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Best Local Similarity 42.44
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                 Matches 100; Conservative
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A,Molecule type: mRNA
A,Residues: 1-638 <RES>
A,Residues: 1-638 <RES>
A,Residues: 1-638 <RES>
C,Coment: This protein, synthesized in the liver, circulates as a noncovalent complex w C,Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a light linked by one or more disulfide bonds.

G, Superfamily: coagulation factor XI; trypsin homology

C;Genetics:

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A;Molecule type: mRNA
A;Residues: 1-275 <VAN>
A;Cresidues: 1-275 <VAN>
A;Cresidues: 1-275 <VAN>
C;Superfamily: trypsin; trypsin; homology
C;Keywords: hydrolase; serine proteinase; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Nolecule type: mRNA
A;Residues: 1-638 <CHU>
A;Cross-treferences: UNIPROT:P03952; GB:M13143; NID:g190262; PIDN:AAA60153.1; PID:g190263
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rivanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 1989
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structural
A;Reference number: A32410; MUID:89352460; PMID:2504277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasma kallikrein (EC 3.4.21.34) precursor - human
N'Alternate names: kininogenin; plasma prekallikrein
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A00921; A37939
R;Chung, D.W.; Pujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four the A;Reference number: A00921; MUID:86243359; PMID:3521732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                      162 DVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTR--RDS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 HVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF--VS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 NIYLSPR-YLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 RIVMHPNYYTPENGADIALLELEDPVNVSAHVQPVTLPPALQTFPTGTPCWVTGWGDVHS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 DEALPSPHTLQEVQVAIINNSMCN---HLFLKYSFR-KDIFGDMVCAGNAQGGKDACFGD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 GTPLPPPFPLKQVKVPIVENSMCDVQYHLGLSTGDGVRIVREDMLCAGNSK--SDSCQGD 223
      178 YIKEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKD----IFGDMVCAGNAQGGKDA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                     tryptase (EC 3.4.21.59) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRL----WDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LVLALALLGSLVPVS----PAPGQALQRV---GIVGGREAPGSKWPWQVSLRLKGQYW-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                             220 CQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWI 267
                                                                                                                             CFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGPLVCRVRGVWLOAGVVSWGEGCAOPNRPGIYTRVAYYLDWIHO 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.1-21/Domain: signal sequence #status predicted <SIG>P:12-30/Domain: activation peptide #status predicted <ACT>P:22-30/Domain: artivation peptide #status predicted <ACT>P:31-275/Product: tryptase #status predicted <AMT>P:31-267/Domain: trypsin homology <TRY:
P:74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.5%; Score 509; DB 2; 40.6%; Pred. No. 4.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.6%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.6
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A32410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:P20231; GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983; NOte: residues 2-275 are derived from mRNA; residue one was inferred from the genomic; Miller, J.S.; MoxLey, G.; Schwartz, L.B.

Clin. Invest. 86, 864-870, 1990

Clin. Invest. 86, 864-870, 1990

;Title: Cloning and characterization of a second complementary DNA for human tryptase.; Reference number: A37193; MUID:90369005; PMID:2203827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cand. J. Hellman, L. Callman, L. Callman, L. J. Mallman, J. 203-208, 1993
cand. J. Immunol. 37, 203-208, 1993
fittle: Characterization of a tryptase mRNA expressed in the human basophil cell line preference number: 159473; MUID:93166209; PMID:8434231
Accession: 159473
scatus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                               Lryptase (EC 3.4.21.59) II precursor - human N;Alternate names: tryptase beta C;Species: Homo sapiens (man) C;Date: O3-Feb-1994 #sequence revision 03-Feb-1994 #text_change 09-Jul-2004 C;Accession: B35863; A37193; I59473 Tam, B.K.; Goldstein, S.M.; Craik, C.S.; Caughey, C R;Vanderslice, P.; Ballinger, S.M.; Tam, B.K.; Goldstein, S.M.; Craik, C.S.; Caughey, C Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990 A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine E A;Reference number: A35863; MUID:90251647; PMID:2187193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11,
                                                                                             DIALLKLTNPVNISDYVHPVPLPPASETFPSGTLCWVTGWGNIDNGVNLPPFFPLKKJVQV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -WDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 YW-MHPCGGSLIHPQWVLTAAHC--VGPDVKDLAALRVQLRE------QHLYYQDQL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VSNIYLSPR-YLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                             197 ALINNSMCNHLFLKYSFRKD----IFGDMVCAGNAQGGKDACFGDSGGPLACNKDGLWYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LILAL--LLARAGIRKPESQEAAPISGPCGRRVITSRIVGGEDAELGRWPWQGSLRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILALPVILASRA-----YAAPAPGQALQRV---GIVGGQEAPRSKWPWQVSLRVHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-275 <RES>
Cross-references: GB:S5551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
Experimental source: basophil cell line KU812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 1-275 <MLL>
Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GDB:125890; OMIM:191080
A;Map position: 16pter-16qter
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Superfamily: signal sequence #status predicted <SIG>F;1-21/Domain: signal sequence #status predicted <SIG>F;2-30/Domain: activation peptide #status predicted <ACT>F;31-257/Product: tryptase I #status predicted <ACT>F;31-267/Domain: trypsin homology <TRY>F;31-267/Domain: trypsin homology <TRY>F;31-267/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.5%; Score 509; DB 2; 39.9%; Pred. No. 4.6e-38; tive 43; Mismatches 92;
                                                                                                                                                                                                                       253 IGVVSWGVGCGRPNRPGVYTNISHHFEWI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA; DNA
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Best Local Similarity
Matches 115; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1-275 <VAN>
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mast cell, it is up

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C; Comment: This enzyme is basically specific for a connective tissue
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Best Local Similarity 39.3%;
Matches 116; Conservative 3:
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Best Local Similarity 38.8%
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A45754
A; Molecule type: mRNA
A; Residues: 1-274 <MIL>
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A;Residues: 1-274 <IDE>
Ą;Cross-references: UNIPROT:P50343; DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID:g5565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Map position: 4q35-4q35
C; Superfamily: cosquiation factor XI; trypsin homology
C; Superfamily: cosquiation factor fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383
F;127,308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status experimental F;318-347,340-345/Disulfide bonds: #status predicted
F;390-391/Cleavage site: Asp. 11e (cogulation factor XIIa) #status predicted
F;34,483,578/Active site: His, Asp, Ser #status predicted
                                                                                                         A, Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.; Maruyama, H.; Osada, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRIVGGINSSWGEWPWQVSLQVKLTAQRHLCGGSLIGHQWVLTAAHCFD---GLPLODV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMVQFG----QLTSMPSFWSLQ--AYYTRYFVSNIYLSPRYLGNSPYDIALVKLSAPVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALPSPHTLQEVQVAIINNSMCNHLF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 LKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGFLACNKDGLWYQIGVVSWGVGCGRPNRP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N'Alternate names: mast cell tryptase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Aug 1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSRIVGGEDAELGRWPWQGSLRL---WDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSG
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R;Ide, H.; Itoh, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maru J. Biochem. 118, 210-215, 1995
A;Title: CDNA sequencing and expression of rat mast cell tryptase. A;Reference number: JC4171; MUID:96015171; PMID:8537314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.3%; Score 507; DB 1; Length 638; Best Local Similarity 39.6%; Pred. No. 1.9e-37; Matches 105; Conservative 43; Mismatches 87; Indels
                                       A;Reference number: A37939; MUID:91152016; PMID:1998666
A;Accession: A37939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Cross-references: GDB:127575; OMIM:229000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVYTNISHHFEWI-OKLMAQSGMSQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tryptase (EC 3.4.21.59) precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388
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A Molecule type: mRNA
A Residues: 1-274 <MI2>
A Consider type: mRNA
A Residues: 1-274 <MI2>
A Conserved to the sequence GB-M30038
A Conserved to the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Pro
C Superfamily: trypsin; trypsin homology
C Superfamily: trypsin; trypsin proteinase; zymogen
C Superfamily: trypsin; proteinase; zymogen
C Superfamily: trypsin sequence #status predicted <SIG>
F;1-21/Domain: activation peptide #status predicted <ACT>
F;1-21/Apmain: trypsin nomology <TRY>
F;31-224/Domain: trypsin homology <TRY>
F;74,120,223/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA for human tryptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRY--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYIKEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKD----IFGDMVCAGNAQGGKD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
A;Title: Cloning and characterization of complementary DNA for human tryptase.
A;Reference number: A45754; MUID:90009311; PMID:2677049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
C;Accession: A45754; B37193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 -MHPCGGSLIHPQWVLTAAHCVGLH--IKSPELFRVQ------LREQYLYYADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 --FVSNIYLSPRYLG-NSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 GDIDSDEPILLPPYPLKQVKVPIVENSLCDRKYHTGLYTGDDVPIVQDGMLCAGNTR--SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LKLLLLLLALSPL--ASLVHAAPC--PVKQRV---GIVGGREASESKWPWQVSLRFKFSFW
einase inhibitors.
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Reywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
C;Rejn-19/Domain: signal sequence #status predicted <ACT>
F;20-29/Domain: activation peptide #status predicted <ACT>
F;30-274/Product: mast cell tryptase #status predicted <AMT>
F;30-236/Domain: trypsin homology <ARS, Ser #status predicted
F;73,120,223/Active site: His, Asp, Ser #status predicted
F;73,120,223/Active site: Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR----LW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LILAL-LLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 ACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 SCQGDSGGPLVCKVKGTWLQAGVVSWGBGCAEANRPGIYTRVTYYLDWIHRYVPQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 274;
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R,Miller, J.S.; MoxLey, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary
A;Reference number: A37193; MUID:90369005; PMID:2203827
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 499; DB 2; Length 274; Pred. No. 3.6e-37; 39; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.8%; Score 498.5; DB 2; Length 38.8%; Pred. No. 4e-37; ive 44; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::
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27.6%; Score 476.5; DB 1;
41.1%; Pred. No. 6.2e-35;
iive 30; Mismatches 96;
                                                                                                                                                                                                                                                             27.7%; Score 478.5; DB 1
40.6%; Pred. No. 6.7e-35;
tive 40; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: GDB:HPN; TMPRSS1; hepsin
A;Cross-references: GDB:135685; OMIM:142440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 19q11-19q13.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepsin (EC 3.4.21.-) - human
                                                                                                                                                                                                                                                                                                    Local Similarity
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Matches 115; Conserv
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A; Residues: 1-417 <LEY>
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                                                                                                                                                                                                                                                                                                                                        102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
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Residues: 28-33;35-49,'X',51-55,'X',57-63;70-75,'X',77-79;107-109,'X',111-112;132-139;
280-282,'X',284,285-297;313-316,'X',318-319;320-326;'X',328-330;'X',347-349;373,'X',375
280-282,'X',284,285-297;313-316,'X',318-319;320-326;'X',328-330;'X',347-349;373,'X',375
280-282,'X',284,285-297;313-316,'X',318-319;320-326;'X',328-330;'X',347-349;373,'X',375
280-282,'X',284,285-297;313-316,'X',517-637;'X',57-637;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;'X',57-797;
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A;Map position: 4435-4435
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 52
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(Crosas references: UNIPROT: P03951; GB:M18295

(Rosas references: UNIPROT: P0308; the authors' translation

(Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.

10chemiastry 25, 2417-2424, 1986

(Tritle: Amino acid sequence of human factor XI, a blood coagulation factor with four reference number: A00920; MUID:86243360; PMID:3636155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      presence
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Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer;
1.1-18/Domain: signal sequence #status predicted <SIG>
1.9-38/Product: coagulation factor XIa heavy chain #status experimental <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 KEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKD----IFGDMVCAGNAQGGKDACF 235
                                                                                                                                                                                                                                                                                                                                                                                                                           VSNIYLSPR-YLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYI 179
54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human
N;Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
LLLALPVLASRAYAAPAPVQALQQAG-----IVGGQEAPRSKWPWQVSLRVKDRY
                                                                           -SHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF--
                                                                                                                      Description: catalyzes the proteolytic activation of coagulation factor Pathway: blood coagulation intrinsic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Location of the disulfide bonds in human coagulation factor XI: ,Reference number: A37940; MUID:91152017; PMID:1998667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:M13142; NID:9182832; PIDN:AAA52487.1; PID:9182833
McMullen, B.A.; Pujikawa, K.; Davie, E.W.
lochemistry 30, 2056-2060, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fitle: Organization of the gene for human factor XI. Reference number: A27431; MUID:88107663; PMID:2827746; Accession: A27431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: Ā27431; A00920; Ā37940
Asakai, R.; Davie, E.W.; Chung, D.W.
ochemistry 26, 7221-7228, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :109-198/Domain: apple repeat <AP2>:199-288/Domain: apple repeat <AP3>:290-379/Domain: apple repeat <AP4>
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Residues: 1-625 <FUJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A00920
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F;46-76,50-56,110-193,136-165,140-146,200-283,226-255,230-236,291-374,317-346,321-327,386
F;99,126,353,450/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;339/Disulfide bonds: interchain #status predicted
F;337-380/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;431,480,575/Active site: His, Asp, Ser #status predicted
F;491/Binding site: carbohydrate (Asn) (covalent) #status experimental transmembrane dome A,Cross-references: UNIPROT:P05981; EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064 œ, 151 KHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALPSPHTLQEVQVAIINNSMCNHLFLK 210 80 AAHCPETYSDLSDPSGWMVQFGQLTSMPSFWSLQ-----AYYTRYFVSNIYLSPRYLGN 133 134 SPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWG---YIKEDEALPSPHT 190 255 S-NDIALVHLSSPLPLTEYIQPVCLPAAGQALVDGKICTVTGWGNTQYYGQQAGV---- 308 C;Species: Homo sapiens (man) C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 16-Aug-2004 C;Accession: S00845 201 AAHCFPERNRVL--SRWRV-FAGAVAQASPHGLQLGVQAVVYHGGYLP---FRDPNSEEN 92 DPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRY-LGNSPYDIALVKLSAPVTYT 494 DSQRPICLPSKGDRNVIYTDCWVTGWGYRKLRDKI--QNTLQKAKIPLVTNBECQK---R YSFRKDIFGDMYCAGNAQGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRPGV 21 PESQEAAPLSGPCGRRVI-TSRIVGGEDAELGRWPWQGSLRLWDSHVCGVSLLSHRWALT 38 ITSRIVGGEDAELGRWPWQGSLRL---WDSHVCGVSLLSHRWALTAAHCF---ETYSDLS Riceytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W. Blochemistry 27, 1067-1074, 1988 A;Title: A novel trypsin-like serine procease (hepsin) with a putative A;Reference number: S00845; WUID:88209431; PMID:2835076 C;Superfamily: trypsin homology C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein F;23-45/Domain: transmembrane #status predicted <TMN> F;163-400/Domain: trypsin homology <TRY> F;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted 23; DB 1; Length 417; DB 1; Length 625; 86; Indels F;203,257,353/Active site: His, Asp, Ser #status predicted

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191 LQEVQVAIINNSMCNHLFLKYSFRKDIFGD-----MVCAGNAQGGKDACFGDSGGPLAC- 244
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Search completed: February 27, 2005, 20:23:27 Job time : 26.5815 secs

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2857, 2857, 2857, 2857, 2857, 2857, 2857, 2857, 2857, 2857, 2857,

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Perfect score:

6

Run

Sequence:

Scoring table:

Searched:

Database

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Sequence 6, Application US/10040647

Substitution No. US20030092154A1

GENERAL INFORMATION:

APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David TITLE OF INVENTION: NOVEL MOLECULES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET 400 GARDEN CITY PLAZA

CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/023,942
APPLICATION NUMBER: 005101/97
FILING DATE: 13-FEB-1997
FILING DATE: 18-P0422/97
FILING DATE: 18-NOV-1997
FILING DATE: 18-P0422/97
FILING DATE: 18-P0421996
FILING DATE: 13-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FAIABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compartible
COMFUTER: TBM FO Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/040,647
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
                  US-09-907-575-257
US-09-905-075-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-902-634-257
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  STATE: NEW YORK
COUNTRY: USA
ZIP: 11530
\begin{array}{c} ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\ ... \\
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PRIOR
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  Sequence 3, Appli
Sequence 257, App
Sequence 14, Appl
Sequence 257, App
                                                                                                                                                                          (without alignments)
1153.685 Million cell updates/sec
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                                                                                                                                                   ; Search time 89.2843 Seconds
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1 MGARGALILIALIJARAGLRK......PSWPLLFFPLLWALPLIGPV 314
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1: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/NGG NEW_PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/USOG NEW_PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/USOG NEW_PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/USOB NEW_PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USOB NEW_PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/USOB NEW_PUB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/USOB NEW_PUB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-968-415-3
US-09-909-320-257
US-09-909-088B-257
US-09-905-291A-257
US-09-905-291A-257
US-09-907-824-257
US-09-907-841-257
US-09-904-011-257
US-09-908-033-257
US-09-908-033-257
                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                               1385339 segs, 328044528 residues
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                                                                                                                                                   2005, 20:22:41
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                     February 27,
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NAME: DIGIGLIO, FRANK S REGISTRATION NUMBER: 31,346

1723 1723 1723 1723 1723 1723 1723 1723

Result No.

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APPLICATION NUMBER: 09/659,151
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                                                                                                                                                                                                                                                                                                                                                1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
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Best Local Similarity 100.0%; Pred. No. 3.7e-159;
Matches 314; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09968415
; Sequence 3, Application US/09968415
; Publication No. US20020086334A1
; GENERAL INFORMATION:
; Hallman, Olga
; Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OP SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: PARTE CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
CCMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,415
FILING DATE: 26-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
REFERENCE/DOCKET NUMBER: 11168
              TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                        LENGTH: 314 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
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61 IMDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 PLACNROGLWYQIGVVSWGVGCGRPNRPGVYTNISHHPFWIQKLMAQSGWSQPDPSWPLL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
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Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0;
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
                                                                                                                                                  TELEPHONE: 650-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 257, Application US/09909320 Patent No. US20020132240A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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CLONE: 789927
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Gerritsen, Mary E
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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241 PLACNKDGLMYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300  
241 PLACNKNGLMYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
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GENERAL INFORMATION:

TITLE OF INVENTION: Regulation of Human Eosinophil Seri;

TITLE OF INVENTION: Protease-1-Like Enzyme
FILE REFERENCE: 04974.00512
CURRENT APPLICATION NUMBER: US 60/212,844
PRIOR APPLICATION NUMBER: US 60/212,844
PRIOR APPLICATION NUMBER: US 60/212,844
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/244,171
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2001-03-30
PRIOR PRIOR PRICATION NUMBER: US 60/279,766
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: S8
SOFTWARE: FASTESEQ for Windows Version 4.0
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99.7%; Pred. No. 1.1e-158;
iive 1; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                    US-09-885-441-14; Sequence 14, Application US/09885441; Sequence 14, Application US/09885441; Setent No. US20020146407A1; GENERAL INFORMATION:
                                                                                                                                                   301 FFPLLWALPLLGPV 314
                                                                                                               FFPLLWALPLIGPY 314
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Best Local Similarity 99.7
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-885-441-14
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US-09-909-088B-257
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                                                                APPLICANT: Stewart, Indichy A.
APPLICANT: Mass, Daniel
APPLICANT: Williams, Daniel
ITILE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-11-04
FILE REFERENCE: 10466-11-04
FILE REFERENCE: 10466-11-04
FRIOR APPLICATION NUMBER: US/09/99320
FRIOR FILING DATE: 1999-07-28
FRIOR FILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-09-15
FRIOR PELLORY NUMBER: PCT/US99/20594
FRIOR PELLORY NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-10-0-15
FRIOR PELLORY NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-10-0-15
FRIOR PELLORY NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-10-0-15
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FRIOR PELLORY NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-10-0-15
FRIOR PELLORY NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-10-0-15
FRIOR PELLORY NUMBER: PCT/US99/20595
FRIOR PELLORY NUMBER: PCT/US99/20595
FRIOR PELLORY NUMBER: PCT/US99/20595
FRIOR PELLORY NUMBER: PCT/US99/20599
FRIOR PELLORY NUMBER: PCT/US99/2
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99.7%; Pred. No. 1.1e-158;
tive 1; Mismatches 0;
                                                          Roy, Margaret Ann
Stewart, Timothy A.
Pan, James
Paoni, Nicholas F.
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Best Local Similarity 99.7
Matches 313; Conservative
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ORGANISM: Homo Sapien
US-09-909-320-257
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241 PLACNKNGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFFWIQKLMAQSGMSQPDPSWPLL 300
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                                                                   61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF
                                                                                                                                                                                                181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
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CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US99/21090
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
Roy, Margaret Ann
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L
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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR FILING DATE: 1099-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-00-08
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
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PRIOR FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/28214
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FILING DATE: 1999-11-30
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FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-20
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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                                             errara, Napoleone
ilvaroff, Ellen
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Gerber, Hanspeter
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father, Jennie P.
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CORGANISM: Homo Sapien
US-09-909-088B-257
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FILING DATE: 1999-09-15

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61 IMDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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Pred. No. 1.1e-158;
1; Mismatches 0;
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CURRENT PAPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR PRIOR PAPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
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PRIOR FILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
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PRIOR PRILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PRILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-10-05
PRIOR PRILING DATE: 1999-10-05
PRIOR PRILING DATE: 1999-10-05
PRIOR PRILING DATE: 1999-11-20
PRIOR PRILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-03
PRIOR PRILING DATE: 1999-12-03
PRIOR PRILING DATE: 1999-12-03
Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
Pan, James
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CORGANISM: Homo Sapien
US-09-902-853-257
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Best Local Similarity
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                                                                                                                   PRIOR FILING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/21547
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Filvaroff, Ellen
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Gerber, Hanspeter
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Goddard, A.
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Best Local Similarity 99.7
Matches 313; Conservative
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Eaton, Dan L.
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Gao, Wei-Qiang
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SEQ ID NO 257
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ORGANISM: Homo Sapien
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Publication No. US20
GENERAL INFORMATION:
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JS-09-907-841-257
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121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
                                                                                                                             241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Screeed and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
                                            EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 1090-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1000 00 1
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28313
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PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/20944
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5. US20020197671A1
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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99.7%; Pred. No. 1.1e-158;
iive 1; Mismatches 0;
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR PELICATION NUMBER: PCT/US99/28565
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: PCT/US99/3091
PRIOR PPLICATION NUMBER: PCT/US99/30911
PRIOR PPLICATION NUMBER: PCT/US99/3091
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PLING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PRIOR PRIOR DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PRIOR PRIOR DATE: 257
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Gerritsen, Mary E.
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Best Local Similarity 99.73
Matches 313; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
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                                                                                       APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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SEQ ID NO 257
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CURRENT APPLICATION NUMBER: US/09/907,841

CURRENT PILING.DATE: 2001-11-20

PRIOR PRIOR TILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-05

PRIOR PILING DATE: 1999-11-29
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ORGANISM: Homo Sapien
US-09-907-841-257
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US-09-904-011-257 ; Sequence 257, Application US/09904011 ; Publication No. US20030003530A1 ; GENERAL INFORMATION:

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APPLICANT: Genetic h. Inc.
APPLICANT: Genetic h. David
APPLICANT: Bockeria. Not.
APPLICANT: Bockeria. Not.
APPLICANT: Bockeria. David
APPLICANT: Bockeria. David
APPLICANT: Bockeria. David
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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99.7%; Score 1723; DB 10; Length 314; 99.7%; Pred. No. 1.1e-158; ive 1; Mismatches 0; Indels 0
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CURRENT APPLICATION NUMBER: US/09/903,640
CURRENT FILING DATE: 2001-07-11
FRIOR APPLICATION NUMBER: 09/665,350
FRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                 Matches 313; Conservative
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Eaton, Dan L.
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ORGANISM: Homo Sapien
US-09-903-640-257
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US-09-903-640-257
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                                                                                                                                      1 MGARGALLIALILIARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWGGSLR
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                          1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
                                                       Gaps
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  Length 314;
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99.7%; Score 1723; DB 10; 99.7%; Pred. No. 1.1e-158;
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                                                     1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/908,093
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
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APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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Publication No. US20030017498A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                           Best Local Similarity 99.7 Matches 313; Conservative
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Eaton, Dan L.
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Gao, Wei-Qiang
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MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR 60
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1.1e-158;
1; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
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PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
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PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-06
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PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-06
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PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-10-09
PRIOR PILING
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 99.7%;
Matches 313; Conservative
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Paoni, Nicholas F
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Gerritsen, Mary E
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Mather, Jennie P
                                                                                                                                Wei-Qiang
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Pred. No. 1.1e-158;
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
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PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
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Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bestsein, David
APPLICANT: Bestsein, David
APPLICANT: Bestsein, David
APPLICANT: Baton, Dan L.
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Best Local Similarity 99.7
Matches 313; Conservative
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US-09-908-093-257
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US-09-906-742-257
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                                                                                                                                                            EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG 240
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                     9
and Transmembrane Polypeptides and Nucleic
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PELICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: US 60/146,222
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
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Publication No. US20030027143A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Botstein, David
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121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
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Pred. No. 1.1e-158;
1; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PRILING DATE: 1999-12-06
PRIOR PRILING DATE: 1999-12-06
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PRIOR PRILING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
PRIOR PRIOR PLING DATE: 1999-12-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 99.7
Matches 313; Conservative
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US-09-906-838-257
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1.1e-158;
1; Mismatches 0;
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENDING DATE: 2000-105
NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/0414
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FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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PRIOR APPLICATION NUMBER: US 60/145,698
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PPLICATION NUMBER: US 60/146,222
                                                                                                                                                                                                                                         toy, Margaret Ann tewart, Timothy A. Tumas, Daniel
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Best Local Similarity 99.7%;
Matches 313; Conservative 1
                                                                                                                    Hillan, Kenneth, J
                                                                                                                                                                                                             aoni, Nicholas F.
Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                         Surmey, Austin L.
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; ORGANISM: Homo Sapien
US-09-907-613-257
                                                                                                                                                                                            James
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241 PLACNROGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGWSQPDPSWPLL 300
                121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
                                                                                                                                    241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
                                                                  EDEAL PSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
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Search completed: February 27, 2005, 20:39:49 Job time : 90.2843 secs

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Sequence 6, Application US/09023942A;
Sequence 6, Application US/09023942A;
Patent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David;
TILLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1728; DB 4; Length 314;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparatible
COMPUTER: IBM FC comparatible
COMPUTER: IBM FC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIPTCATION DATA:
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATPONEY/AGENT INFORMATION:
NAME: DIGGILO, FRANK S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
US-09-905-381A-263
US-09-906-618-263
US-08-978-404B-8
US-08-978-404B-21
US-08-978-404B-21
US-09-016-366A-19
US-09-016-366A-19
US-09-016-366A-19
US-08-016-366A-19
US-08-016-366A-19
US-08-078-404B-14
US-08-078-404B-16
US-09-016-366A-21
US-09-016-366A-21
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US-09-016-366A-21
US-09-016-366A-21
US-09-016-366A-21
US-09-016-366A-21
US-09-016-368-16
US-10-177-661-2
US-10-177-661-2
US-09-016-366A-23
US-09-016-366A-23
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
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     TOPOLOGY:
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        Sequence 257, App
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Sequence 3, Appli
                                                                                                                                                                                           February 27, 2005, 20:12:15; Search time 30.0958 Seconds (without alignments) 778.839 Million cell updates/sec
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1728
1 MGARGALLLALLARAGIRK......PSWPLLFFPLLWALPLIGPV 314
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-008-271A-3
US-09-907-775A-257
US-09-905-125A-257
US-09-906-700-257
US-09-906-700-257
US-09-906-708-257
US-09-906-64-257
US-09-906-64-257
US-09-906-64-257
US-09-906-648-257
US-09-906-648-257
US-09-906-648-257
US-09-906-648-257
US-09-906-648-257
US-09-9186-642-34
US-09-023-942A-4
US-09-023-942A-4
US-09-386-642-3
US-09-386-653A-7
US-09-386-653A-7
US-09-386-653A-7
US-09-386-642-11
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US-09-906-700-263
US-09-903-603A-263
US-09-904-920A-263
US-09-909-064-263
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9-902-775A-263
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Result No. 

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IMMEDIATE SOURCE:
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APPLICANT:
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                                                                        1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
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                                                   1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
                   0; Gaps
                   Indels
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COMPOTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASISERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
   Pred. No. 1.1e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tow Y.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 314 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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100.08;
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COMPUTER READABLE FORM
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                 Matches 314; Conservative
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 Best Local Similarity
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APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Aun
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/09/907,794A
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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0
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Pred. No. 3.5e-165;
1; Mismatches 0;
                       CLONE: 789927
SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
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Grimaldi, Christopher J.
                                                                                                                                    99.7%;
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Filvaroff, Ellen
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Gerritsen, Mary E
PROSTUT03
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Hillan, Kenneth,
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Mather, Jennie P.
                                                                                                                                    Query Match
Best Local Similarity 99.73
Matches 313; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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                                                                            US-09-008-271A-3
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APPLICANT: WOOSO, MILISAM, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PLICATION NUMBER: US/09/905,125A

CURRENT FILING DATE: 2001-07-12

PRIOR PELING DATE: 2000-02-22

PRIOR PELING DATE: 1099-07-07

PRIOR PLING DATE: 1099-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-01

PRIOR PLING DATE: 1999-09-01

PRIOR PLING DATE: 1999-09-01

PRIOR PLING DATE: 1999-09-01

PRIOR PLING DATE: 1999-09-11

PRIOR PLING DATE: 1999-09-01

PRIOR PLING DATE: 1999-09-01

PRIOR PLING DATE: 1999-10-12

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PRIOR PLING DATE: 1999-10-12

PRIOR PLING DATE: 1999-10-12

PRIOR PLING DATE: 1999-10-20

PRIOR PLING DATE: 
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
                                                                                      Ferrara, Napoleone
Filvaroff, Ellen
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Gao, Wei-Qiang
Gerber, Hanspeter
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Best Local Similarity 99.7
Matches 313; Conservative
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SEQ ID NO 257
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TYPE: PRT
CRGANISM: Homo Sapien
US-09-905-125A-257
                                                                                                                                                                                                                                                                         Goddard,
                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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Pred. No. 3.5e-165;
1; Mismatches 0;
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PRIOR FILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PLILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
                                                                                                                      APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
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FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                  APPLICATION NUMBER: PCT/US99/20944
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60/145,698
                                                            PLICATION NUMBER: US 60/146,222
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Sequence 257, Application US/09905125A
Fatent No. 6664376
GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 313; Conservative
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ORGANISM: Homo Sapien
US-09-907-794A-257
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APPLICANT: Genentech, Inc

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                                                                              LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
                                                                                                                     61 LWDSHVCGVSLLSHRWALTAAHCPETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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                          EDBALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Gao, Wei-Qiang
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Eaton, Dan L.
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61 LWDSHVCGVSLLSHRWALTAAHCPETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PLILING DATE: 2000-01-05
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Botstein, David
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Best Local Similarity 99.7
Matches 313; Conservative
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Eaton, Dan L.
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US-09-902-775A-257
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US-09-906-700-257
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LENGTH: 314
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241 PLACNKNGLMYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
                             121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
                                                                                                                                         181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG 240
                                                                                                                                                                                           241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFFWIQKLMAQSGMSQPDPSWPLL 300
121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                              EDEAL PSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
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FILE REFRENCE: GWE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-18
APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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PELLING DATE: 1999-07-28
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 277, Application US/09903603A Patent No. 6767995 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Makher, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
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Gao, Wei-Qiang
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Eaton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
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Pred. No. 3.5e-165;
1; Mismatches 0; Indels (
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PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-11-29
PRIOR PELLOGATION NUMBER: PCT/US99/28313
PRIOR PELLING DATE: 1999-11-30
PRIOR PELLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILLING DATE: 1999-12-02
PRIOR APLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/3095
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PRIOR APPLICATION WUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 314
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PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
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TITING DATE: 1999-09-15
TITING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/23089
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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                                            Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                                                                                                                     Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                       Gurney, Austin L.
Hillan, Kenneth, J.
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Gerritsen, Mary E.
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Mather, Jennie P.
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Best Local Similarity 99.7°
Matches 313; Conservative
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ORGANISM: Homo Sapien

US-09-906-700-257
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61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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Pred. No. 3.5e-165;
1; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/904,920A

CURRENT PILING DATE: 2001-01-33

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1909-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

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PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

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PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1
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                                                                                         APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted an
TITLE OF INVENTION: Acids Enco
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Best Local Similarity 99.7
Matches 313; Conservative
                                                              Tumas, Daniel
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US-09-904-920A-257
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Pred. No. 3.5e-165;
1; Mismatches 0; Indels
             PRIOR TILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR FLING DATE: 1999-12-02
PRIOR FLING DATE: 1999-12-05
PRIOR FLING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR PRILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PRILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
APPLICATION NUMBER: PCT/US99/28564
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Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P
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Best Local Similarity 99.73
Matches 313; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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ORGANISM: Homo Sapien
US-09-903-603A-257
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241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300 EDEAL PSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG

Gaps ; 0

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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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99.7%; Pred. No. 3.5e-165;
iive 1; Mismatches 0;
  PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
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Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 99.7
Matches 313; Conservative
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Gao, Wei-Qiang
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                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo Sapien
US-09-909-064-257
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
241 PLACNKNGLWYQIGVVSWGVGCGRPNRPGVYTNISHHPEWIQKLMAQSGMSQPDPSWPLL 300
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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FRIOR PEDLICATION NUMBER: US 60/146,222
RIOR FILING DATE: 1999-07-28
RIOR APPLICATION NUMBER: PCT/US99/20594
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RIOR APPLICATION NUMBER: PCT/US99/20944
RIOR FILING DATE: 1999-09-13
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FILING DATE: 1999-11-29
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                                                                                                                                                                                                                             Sequence 257, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
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                                                                        301 FFPLLWALPLLGPV 314
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Hillan, Kenneth.
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Ashkenazi, Avi
Botstein, David
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57, Application US/09906618
6828146
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Gao, Wei-Qiang
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99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels (
                                            PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
                                                                                                                                                                                                                                                                   DR FILING DATE: 1999-09-08

RAPLICATION NUMBER: PCT/US99/20944

DR FILING DATE: 1999-09-13

R APPLICATION NUMBER: PCT/US99/21090

R FILING DATE: 1999-09-15

DR APPLICATION NUMBER: PCT/US99/21547

PRELING DATE: 1999-09-15
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PRIOR FLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 257
LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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ORGANISM: Homo Sapien
US-09-905-381A-257
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RESULT 11

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                                                                                                                                                         FILE REFERENCE: 1046-14

CURRENT APPLICATION NUMBER: US/9996,618

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-01

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-07

PRIOR PLING DATE: 1999-10-07

PRIOR PLING DATE: 1999-11-29

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PRIOR PLING DATE: 1999-11-20

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PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-12-00

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

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ORGANISM: Homo Sapien
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Sequence 53, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
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89.3%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
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Best Local Similarity 89.3
Matches 260; Conservative
                                                                                                                                                                Conservative
                                                                        ; MOLECULE TYPE: protein US-09-023-942A-4
                                                                                                                           Query Match
Best Local Similarity
Matches 312; Conserva
                                                         linear
                                       TYPE: ami
TOPOLOGY:
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-09-386-642-53
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                                                                                                                                                                               LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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                                                                                                                                                                                                                                                    VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
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                                                                                                                                                                                                                                                                                                                                                                                                241 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFFWIQKLMAQSGMSQPDPSWPLL 300
                                                                                                                                             9
                                                                                                        1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
                                                                                                                                        1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
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                                                                          Gaps
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APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
                                       DB 4; Length 314;
                                                                      0; Indels
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APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                 Score 1723; DB 4;
Pred. No. 3.5e-165;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/023,942A
FILLING DATE: 13-FEB-1998
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REPERENCE/DOCKET NUMBER: 11168
TELECOMMINICATION INFORMATION:
TELEPHONE: (516) 742 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09023942A Patent No. 6479274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
                                   99.7%;
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                   Query Match
Best Local Similarity 99.7
Matches 313; Conservative
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SOFTWARE: Patentl
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US-09-906-618-257
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61 LWDSHVCGVSLLSHRWALTAAHCFET--DLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
   Length 312;
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Pred. No. 4.4e-134;
Score 1706; DB 4;
Pred. No. 1.8e-163;
0; Mismatches 0;
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APPLICANT: Qi. Jenson
APPLICANT: Qi. Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 53
LENGTH: 306
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120 YNNFIQPICLINSTYKFENRTDCWVTGWGAIGEDESLPSPNTLGEVQVAIINNSMCNHMY 179
                                                                                                   180 KKPDFRINIMGDMVCAGTPEGGKDACFGDSGGPLACDQDTVWYQVGVVSWGIGCGRPNRP 239
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                                                                          209 LKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKDGLWYQIGVVSWGVGCGRPNRP
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                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jian-shen
TITLE OF INVENTION: DNA encoding the novel human serine;
TITLE OF INVENTION: protease T
FILE REFERENCE: ON-1032
CURRENT APPLICATION NUMBER: US/09/386,653A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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le : 31.0958 secs
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Best Local Similarity 42.6%
Matches 123; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                           RESULT 15
US-09-386-653A-7
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       128 SPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP 187
                                                                                                      188 SPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNK 247
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: (US ONLY) ANTALIS TONI Marie and HOOPER JOHN David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.4%; Score 1113.5; DB 4; Length 285; 69.1%; Pred. No. 7.3e-104; tive 35; Mismatches 50; Indels 3;
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: BM PC Compatible

COMPUTER: BM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,942A

FILING DATE: 13-FEB-1998

CLASSIFICATION DATA:

APPLICATION NUMBER: PO5101/97

FILING DATE: 13-FEB-1997

PRIOR APPLICATION NUMBER: PP0422/97

FILING DATE: 18-NOV-1997

PRIOR APPLICATION NUMBER: International PCT Application

FILING DATE: 13-FEB-1998

ATTOMNEY/AGENT INPORMATION:

NAME: DIGIGLIO, FRANK S
                                                                                                                                                                                                                                                                                      US-09-023-942A-26
; Sequence 26, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION. ANTALIS TONI
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REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
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IELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
TUDENTH: 285 amino
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Best Local Similarity 69.1%
Matches 197; Conservative
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N-PSDB; AAV59119.
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Aay06434 Human pro
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Aab12132 /
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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## ALIGNMENTS

Serine protease; regulation; cell activity; viability; HELA2; ATC2; BCOM3; testisin; fertility; suppressor; testicular germ cell cancer; seminoma; testis-specific expression; antitumour; sperm development; Amino acid sequence of long isoform of HELA2 AAW77297 standard; protein; 314 AA

97AU-00005101. 97AU-00000422.

New serine protease(s) and kinase involved in regulating cell activity and viability - particularly the testis-specific protease HELA2 used for modulation of fertility and as tumour suppressor.

Claim 3; Page 62-64; 167pp; English.

The present sequence represents the amino acid sequence of the long isoform of HELA2. cDNA generated from HeLa cells and PA1-2 expressing HeLa cells was amplified using PCR primers AAV48312-13. Three new sequences were detected in the 480 bp amplicon. These sequences are designated HELA2 and ATC2 which have high homology to serine proteases and BCCM3 which has homology to a kinase. The proteins are involved in or associated with regulation of cell activity and/or viability. Administration of recombinant HELA2 (also called testisin) is used to increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is

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              expressed in some non-testicular cancers (of colon, pancreas, prostate and ovary), so is a marker/potential therapeutic target for cancer. The promoter from the HELA2 gene is seful for testis-specific expression of other genes, e.g. for gene therapy or modulation of fertility. Drugs that block activity of HELA2 should have antitumour activity (other than in testis) while in testis are ecombinant HELA2 should stop growth of tumours and normalise sperm development (eliminating the need for orchidectomy). Identification of mutant forms of HELA2 can be used to diagnose
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testicular germ cell cancers (seminoma) and is also
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100.0%; Pred. No. 5.9e-147;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 314; Conservative
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18-NOV-1997;
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The present sequence represents the amino acid sequence of the short isoform of HELA2. CDNA generated from HeLa cells and PAI-2 expressing tells was amplified using PCR primers AAV8312-13. Three new sequences were detected in the 480 bp amplicon. These sequences are designated HELA2 and ATC2 which have high homology to serine proteases are designated HELA2 and ATC2 which have high homology to serine proteases and BCOM3 which has homology to a kinase. The proteins are involved in or associated with regulation of cell activity and/or viability. All of also as uppressor of testicular activity and/or viability. HELA2 is also a suppressor of testicular germ cell cancers (seminoma) and is also expressed in some non-testicular cancers (of colon, pancreas, prostate or over the HELA2 gene is useful for testis-specific expression of promoter from the HELA2 gene is useful for testis-specific expression of other genes, e.g. for gene therapy or modulation of fertility. Drugs that thock activity of HELA2 should have antitumour activity (other than in testis) while in testis recombinant HELA2 should stop growth of tumours and normalise sperm development (eliminating the need for orchidectomy).
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                          New serine protease(8) and kinase involved in regulating cell activity and viability - particularly the testis-specific protease HELA2 used for modulation of fertility and as tumour suppressor.
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Pred. No. 1.7e-146;
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                                                                                                         Claim 2; Fig 6; 167pp; English
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N-PSDB; AAV59118.
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/note= "putative mature protein"
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                                                                                                                                                                                               protease is useful in drug compositions for the prevention and treatment of allergic diseases, infectious diseases, tumour diseases, granulomatous diseases, collagen diseases and vascular inflammation
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                                                                                                                                    New eosinophils serine protease - useful for prevention and treatment of allergic, infectious, tumor, granulomatous and collagen diseases.
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                                                                                                                                                                                      The present sequence represents a human eosinophil serine protease. The
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                                                                                                                                                                  Claim 1; Page 9-10; 18pp; Japanese.
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Matches 313; Conservative
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                                                                                                        WPI; 1999-183825/16.
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                                                                                                                  N-PSDB; AAX15336
                                                                                                                                                                                                                                     Sequence 314 AA;
         JP11032768-A.
                                              16-JUL-1997;
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'note= "protein kinase C phosphorylation site"
                                                                  'note= "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                  'note= "casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human protease molecules useful in the treatment of disorders and/or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.7%; Score 1723; DB 2; 99.7%; Pred. No. 1.7e-146; ive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "casein kinase II
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                                                                                                         241 PLACNROGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAGSGMSQPDFSWPLL 300
       LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
                                                                                                 PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
                                                                                                                                                                                                                                            Secreted protein; transmembrane protein; human; enterocolitis; Collinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK
                                                                  EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMYCAGNAQGGKDACFGDSGG
                                    VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWYTGWGYIK
                                                                                EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
                                                                                                                                                                                                                               Amino acid sequence of protein PRO303.
                                                                                                                                                                                 AAY13388 standard; protein; 314 AA
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9705-0059117P.
9705-0059121P.
9705-0059124P.
9705-0059184P.
9705-0059184P.
9705-0059184P.
9705-0062185P.
9705-0062286P.
9705-00622814P.
9705-0063186P.
9705-0063121P.
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28-OCT-1997;
28-OCT-1997;
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ANY13344-403 represent secreted and transmembrane human proteins. The CDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal kindey, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, cropinglus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous call carcinoma of the vulva and gliomas), potent effects on cell growth and queloment, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring, PRO264 can be used as a target for anti-tunor drugs. PRO253 may be used in the treatment of Usber Syndrome or Atrophia areata; PRO269 can be used as anti-thrombotic agent; PRO287 polypeptides and portions may be used for treating problems of the kidney, uterus, endometrium, can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDFSGWNVQFGQLTSMPSFWSLQAYYTRYF 120
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Best Local Similarity 99.7%; Pred. No. 1.7e-146;
Matches 313; Conservative 1; Mismatches 0; Indels
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97US - 0063550P
97US - 0063764P
97US - 0063704P
97US - 0063734P
97US - 0063734P
97US - 0063738P
97US - 0064215P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI, Gurney AL,
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                                                                                    29-OCT-1997
29-OCT-1997
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11-NOV-1997
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28-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell activity, haematopoissis activity, immune stimulating or suppressing activity, haematopoissis activity, issue growth activity, haematopoissis activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour
240
                                                           241 PLACNKNGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
                                                                                        PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
                                                                                                                                                                                                                                                                                                                 proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotatic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
                                            EDEAL PSPHTLQEVQVAI INNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGG
                                                                                                                                                                                                                                                                                   Hydrophobic domain protein from clone HP03116 isolated from KB cells.
                                                                                                                                                                                                                                                                                                        secreted protein; membrane protein; hydrophobic domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 238-240; 410pp; English.
                                                                                                                                                                                                                AAB12132 standard; protein; 314 AA
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98JP-00364315.
99JP-00069811.
99JP-00119299.
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                                                                                                                                    FFPLLWALPLLGPV 314
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N-PSDB; AAA62005, AAA62015.
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(PROT-) PROTEGENE INC.
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19-MAY-1999;
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22-DEC-1998;
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     for
inhibition activity. The present protein could therefore be used f
treatment of autoimmune disease, Alzheimer's disease, Parkinson's
disease, and cancer
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                                                                                                                                                     Score 1723; DB 3;
Pred. No. 1.7e-146;
1; Mismatches 0;
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Matches 313; Conservative
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                                                                                                         Sequence 314 AA;
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                                                                                                                                                       Query Match
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Yuan J;
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                                                                                                                                                    The polypeptides and polymucleotides of the invention may be useful as research tools and as therapeutics for treating entercolitis, Zollinger-Blison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal ecarting and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, ALDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                    Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
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                                                                                                                                    invention relates to a novel nucleic acid encoding a PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangogenic; vasotropic; antiasthmatic; antiatic; cancer; antiathritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                             Claim 12; SEQ ID NO 257; 355pp; English
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                                                                                                                                                                                                                                                                                                                                                      PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 99.7 es 313, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 314 AA;
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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, eardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), inflammatory pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LWDSHVCGVSLLSHRWALTAARCRETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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n ME, Goddard A;
Kljavin IJ;
Tumas D;
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99WO-US028313.
99WO-US028564.
99WO-US028565.
99WO-US03095.
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99US-0146222P.
99WO-US020594.
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99WO-US021090.
99WO-US021547.
99WO-US023089.
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2000WO-US000219
                             22-FEB-2000; 2000WO-US004414
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15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
30-NOV-1999;
02-DEC-1999;
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16-DEC-1999;
                                                                                                                                                 28-JUL-1999
08-SEP-1999
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Sequence 314 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TADG-16 contains the conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence characteristic of the serine protease family. An antiesnse oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer. TADG-16 protein or its fragments are useful for vaccinating an individual against TADG-16. Numerous TADG-16 peptides (AAU02225-AAU02384) are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA B27, HLA B8, HLA B2702, and HLA B4403
             241 PLACNKNGLWYQIGVVSWGVGCGRPNRPGVYTNISHHPEWIQKLMAQSGMSQPDPSWPLL 300
PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease, tumour antigen derived gene-16 (TADG-16) protein. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas
                                                                                                                                                                                                                      Human, extracellular serine protease, tumour antigen derived gene-16, TADG-16, ovarian carcinoma, breast cancer; lung cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tumor antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Region containing Ser residue of conserved catalytic triad found in serine proteases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a novel human extracellular serine
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                                                                                                                                                                                                                                                                                                                                                                                                     conserved
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catalytic triad found in serine proteases"
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/label= Signal_secretion_sequence
                                                                                                                                                                                                                                                                                                                                18. .314
/label= Secreted_TADG-16_protein
                                                                                                                                                                                               Human extracellular serine protease TADG-16
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                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                             AAU02223 standard; protein; 314 AA
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                                                             FFPLLWALPLLGPV 314
                                              FFPLLWALPLLGPV 314
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                                                                                                                                                                                                                                                prostate cancer; HLA type.
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                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                    AAU02223;
                                                                                                                                                                                                                                                                                              Key
Peptide
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                                                                                                                                                                                                                                                          61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        PLACNKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFFWIQKLMAQSGMSQPDPSWPLL 300
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                                                                                                                                                                    1 MGARGALILIALIARAGIRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDEAL PSPHTLQEVQVAI INNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
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                                                                                                                                1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR
                                                                        Gaps
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         Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human eosinophil serine protease-1 (esp-1) like enzyme #2.
                                                                 Indels
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Score 1723; DB 4;
Pred. No. 1.7e-146;
1; Mismatches 0;
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31-OCT-2000; 2000US-0244171P.
30-MAR-2001; 2001US-0279766P.
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                                    99.78;
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   Query Match
Best Local Similarity 99.7
Matches 313; Conservative
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15-OCT-1997;
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05-JAN-2000;
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 diagnostic value. Espl-like enzyme modulator is useful for treating espl-like enzyme dysfunction related diseases condition such as asthma, airway allergy, chronic obstructive pulmonary disease (COPD) or osteoporosis. Esp-1 like enzyme is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to presence of mutations in the nucleic acid sequences which encode the enzyme. Pharmaceutical composition comprising esp-1 like enzyme is useful for treating dermatitis, Paget's disease, and preventing degradation of bone implants particularly dental implants. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO; secreted polypeptide; transmembrane polypeptide; pathological disorder; cardiac insufficiency disorder; protein secretion; pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis; skin disease; keratinocyte differentiation; epithelial cancer; tumour; lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma; cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal; antiulcer; dermatological; vulnerary.
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                                                                                                                                                                                                                                                                                                                                                                                            PLACNKDGLWYQ1GVVSWGVGCGRPNRPGVYTN1SHHFEW1QKLMAQSGMSQPDPSWPLL
 assays to identify test compounds with potential therapeutic or
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                                                                                                                                                            99.7%; Score 1723; DB 5; Length 314; 99.7%; Pred. No. 1.7e-146; ive 1; Mismatches 0; Indels (
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97US-0059117P.
97US-0059119P.
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                                                                                                                                                                       Best Local Similarity 99.7
Matches 313; Conservative
                                                                                                                esp-1 like enzyme
                                                                                                                                        Sequence 314 AA;
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17-SEP-1997;
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9705-005228P-
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9705-0053816P-
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98WO-US019177.
98WO-US019330.
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2000WO-US004414.
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99WO-US028313
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Human, secreted and transmembrane protein; PRO polypeptide; cancer;
Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
neuroprotective.
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97US-0063121P.
97US-0063127P.
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9705-0063327P-
9705-0063541P-
9705-0063542P-
9705-0063548P-
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9705-0063732P-
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97US-0063870P.
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9705-00592659-
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97US-0066364P.
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99WO-US021547
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               Human PRO polypeptide #45
                                                                                                                                JS2002192659-A1.
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13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
                                                                                                   Homo sapiens.
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18. SEP - 1997

18. SEP - 1997

18. SEP - 1997

19. SEP - 1997

17. OCT - 1997

24. OCT - 1997

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21-NOV-1997;
24-NOV-1997;
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 The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polymuclectides encoding them. The PRO polypeptides and polymuclectides can be used in treating pathological disorders and tumnours, in therapeutic treatment of cardiac insufficiency secretion by the pancreas, including diabetes. They can also be used in treating disorders associated with the preservation and maintenance of treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriases, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulya and gliomas).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences can be used as molecular markers for protein electrophoresis purposes and can be utilised in protein-protein binding assays, blochemical screening assays, immunoassays and cell-based assays. This sequence represents a human PRO polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGARGALLLALLLARAGIRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR 60
                                                                                                                                                                                                    Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.
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                                                                    Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Macher JP, Pan P, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Mood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.7%; Score 1723; DB 6; Length 314; 99.7%; Pred. No. 1.7e-146; tive 1; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                Claim 12; Fig 92; 473pp; English.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.7
Matches 313; Conservative
                                          (GETH ) GENENTECH INC
                                                                                                                                                          WPI; 2003-328338/31.
N-PSDB; ACA59107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 314 AA;
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181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG
                                             PLACNXDGLWYQIGVVSWGVGCGRPNRPGVTTNISHHPEWIQKLMAQSGMSQPDPSWPLL
                                                                                       241 PLACNINGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, secreted protein, transmembrane protein, PRO, gene therapy, chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane protein PRO303.
                                                                                                                                                                                                                                                                                                   ABU71935 standard; protein; 314 AA.
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970S-0059115P
970S-0059115P
970S-0059121P
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970S-005926P
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970S-0062814P
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97US-0065186P.
97US-0065846P.
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                                                                                                                                       FFPLLWALPLLGPV 314
                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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ABU71445-ABU71505 represent human PRO polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
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                       99WO-US028214.
99WO-US028313.
99WO-US028301.
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99WO-US028565.
99WO-US030095.
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2000WO-US000219.
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2000WO-US014042.
2000WO-US015264.
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24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
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2000WO-US007377
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Best Local Similarity 99.7'
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-361832/34.
N-PSDB; ACA58504.
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11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
02-MAR-2000;
20-MAR-2000;
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01-DEC-1999;
02-DEC-1999;
16-DEC-1999;
16-DEC-1999;
20-DEC-1999;
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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 8 secteted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal comprising a PRO polypeptide of fused to a PRO polypeptide lacking its associated signal petterologous amino acid sequence, an anti-PRO antibody, detecting a PRO245 or PRO1868 and modulating at least one biological activity of a cell expressing a PRO245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, in generating probes and in tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ". Coccett D' Desnoyers L' Eaton DL, Pong S, Gao W, Gerber H, Gerritsen Crimaldi JC, Gurney AL, Hillan KJ, Pan J, Paoni NF, Roy MA, Stewart TA, Wood WI;
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                                                                                                                                                                                                                                                                                                                 99WO-US028565.
99WO-US030095.
99WO-US030911.
                                                    97US-0066466P.
97US-0066511P.
97US-0066770P.
97US-0066772P.
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2000WO-US005004.
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98WO-US019177.
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2000WO-US007377.
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98WO-US025108
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Filvaroff E,
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24-AUG-2000;
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Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D;

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transgenic animals or knock-out animals which may be used to generate either transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural
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Alzheimer's disease; inflammation; nephritis; wound healing;
nerve repair; collateral blood vessel formation; cancer;
colorectal cancer; haemorrhage; rheumatonid arthritis; diabetes;
circhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
infertility; gene therapy.
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                                                                                                                                                                                                                                                                           99.7%; Score 1723; DB 6; Length 314; 99.7%; Pred. No. 1.7e-146;
                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                    The present sequence represents a PRO protein
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                                                                                                                                                                                                                                                                                                                   1; Mismatches
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97US-0059115P.
97US-0059117P.
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                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                         Sequence 314 AA;
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17-SEP-1997;
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97US-0059268P

97US-0062128P

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97US-0063112P

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24-OCT-199,
24-OCT-1997;
24-OCT-1997
7-OCT-1997
                                                       17-0CT-1997;
21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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18-SEP-1997;
15-OCT-1997;
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301 FFPLLWALPLLGPV 314

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EDEAL PSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG

181 181 241

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120 180 180

9

Gaps

0;

5; Length 314; 16; Indels

99.7%; Score 1723; DB 6; 99.7%; Pred. No. 1.7e-146; iive 1; Mismatches 0;

Query Match Best Local Similarity 99.7° Matches 313; Conservative 61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYF 120

61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDFSGWMVQFGQLTSMPSFWSLQAYYTRYF 121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK

1 MGARGALLIALILARAGIRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR

8 8 8 8

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MGARGALLLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR

121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK

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The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 20928B), or a sequence
with at least 80% identity to a DNA encoding a PRO polypeptide comprising
any of 61 sequences having 164-1119 amino acids fully defined in the
specification. The PRO polypeptides or polymuclectides are useful as
pharmaceuticals, diagnostics, biosensors or bioreactors. These are
particularly useful for detecting or treating e.g. Parkinson's disease,
Alzheimer's disease, inflammations, nephritis, wound healing, nerve
cc particularly useful for detecting or treating e.g. colorectal
cancer), haemorrhage (or reduce risk for hemorrhage), rheumatoid
arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
csetenosis, dermal fibrotic conditions (e.g. keloids or scarring),
ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
infertility and markers, or for chromosome identification. The PRO
cc genes are useful as hybridisation probes, or for screening libraries of
human cDNA, genomic DNA or mNAA. The PRO genes may also be used in gene
therapy, particularly for replacing a defective gene This is the amino
claid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                             New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
                                                                                                                                                  Ferrara N;
n ME, Goddard A;
Kljavin IJ;
                                                                                                                                                                                                                                Tumas D;
                                                                                                                                                  Botstein D, Desnoyers L, Eaton DL, Pong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ, an J, Paoni NF, Roy MA, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 92; 482pp; English
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
                                                                                                                                                                                                                                                     Wood WI;
                                                                                                   GETH ) GENENTECH INC.
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N-PSDB; ACD07611.
                                                                                                                                                                                                                           Pan J,
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Filvaroff E, F
Godowski PJ, G
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Williams PM,
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PPPLLWALPLIGPV 314

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Human; PRO; secreted protein; transmembrane protein; enterocolitis; gastrointestinal ulceration; skin disease; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; sequamous cell carcinoma; Alzheimer's disease; Parkinson's disease; rheumatophic lateral sclerosis; inflammatory disease; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; diseatic adjing; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; wound repair.
                                                                             Human secreted/transmembrane protein PRO303
                   ABU54391 standard; protein; 314 AA.
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970S-0063435P.
970S-0063435P.
970S-0063732P.
970S-0063734P.
970S-00637335P.
970S-00637338P.
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970S-0059113P.
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970S-0059121P.
970S-0059121P.
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970S-0062185P.
970S-0062188P.
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9705-0062816P.
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97US-0064809P.
97US-0065186P.
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97US-0063549P.
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                                                          10-MAR-2003 (first entry)
                                                                                                                                                                                                                   US2002132240-A1.
                                                                                                                                                                                                 Homo sapiens.
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21-0CT-1997;
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RESULT 15
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9703-0066453P.
9703-0066466P.
9703-0066511P.
9703-0066770P.
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2000WO-US007377.
2000WO-US008439.
2000WO-US014042.
                                                                                                    99WO-US028313.
99WO-US028301.
99WO-US028564.
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                                          98WO-US018824
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2000WO-US005004
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                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                          16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
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24-FEB-2000;
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13-SEP-1999;
15-SEP-1999;
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17-SEP-1998;
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29-NOV-1999
                                                                                                    30-NOV-1999
                                                                                                                    02-DEC-1999
                                                                                     15-SEP-1999
                                     24-NOV-1997
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-147434/14. N-PSDB; ABX71659.

ö New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease

Claim 12; Fig 92; 473pp; English

The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) any one of 61 fully defined amino acid sequence given in the specification (appearing as ABUS4407).

ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence deposited under American Type Culture Collection (accession numbers is acksociated signal peptide; (d) an extracellular domain of the PRO sequences which lacks its associated signal peptide; (d) an extracellular domain of the PRO polypeptide with its associated signal peptide; or (e) an extracellular domain of the PRO polypeptide which lacks its associated signal peptides. Also include are the nucleic acids encoding the PRO polypeptides and nucleic acids are useful in diagnosing or treating of polypeptides and nucleic acids are useful in diagnosing or treating anterocolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzhaimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.

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cc rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosals, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The cajing, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein cleatrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. The present sequence
              88888888888888888888888888
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Sequence 314 AA;

EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG 240 61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWWVQFGQLTSMPSFWSLQAYYTRYF 120 121 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180 VSNIYLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGG 240 PLACHKDGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLL 300 1 MGARGALILAALALARAGLRXPESQEAAPLSGPGGRRVITSRIVGGEDAELGRWPWQGSIR 60 1 MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLR 0; Gaps 99.7%; Score 1723; DB 6; Length 314; 99.7%; Pred. No. 1.7e-146; Live 1; Mismatches 0; Indels C Query Match Best Local Similarity 99.7' Matches 313; Conservative 19 181 181 셤 셤 g ઠે à ò g à ð

Search completed: February 27, 2005, 20:22:32 Job time: 118.374 secs

FFPLLWALPLLGPV 314

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241 PLACNKNGLWYQIGVVSWGVGCGRPNRFGVYTNISHHFFWIQKLMAQSGMSQPDPSWPLL 300

25 444.2 40.4 510 4 BM759973 BM759973 K-EST0040  2 24 41.6 40.1 462 1 A1016399 CR735731 CR735731 CR735731  2 2 440.4 40.0 463 7 CR735731 AA525010 A1016399 CW59h09.8  2 3 414.2 37.7 1018 6 BY706352 BY706352 BY706352 CR735731 CR735732 CR73572 CR735732 CR73572	ALIGNMENTS . RESULT 1	LOCUS CR590593 LOCUS DEFINITION Full-length CDNA clone CSODEO10YPOS of Placenta of Homo sapiens (human). ACCESSION CR590593 CR590593.1 GI:50471400 KEYWORDS FUC; CNSLT_CDNA. GR690593.1 GI:50471400 KEYWORDS HOMO sapiens UNEATOVE; Heazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE I (bases I to 1077) AUTHORS Lii, W.B., Gruber, C., Jessee, J. and Polayes, D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished Contact: Feng Liang Email: fliang@lifetech.com URL:	http://tuillength.invitrogen.com/ invitroger Paraday Avenue (Jases 1 to 1077) Genoscope. Direct Submission	Submitted (2 B 191 91006 B P 191 91006 B E B E B WWW. 18t B E E B B B B B B B B B B B B B B B B	source 1lu// /organism="Homo sapiens" /mol_type="mRNA" /db xref="taxon:9666" /clone="CSOBE010yPO5" /tissue_type="placenta" /plasmid="pcMVSPORT_6"	Query Match         97.4%;         Score 1071.8;         DB 3;         Length 1077;           Best Local Similarity         99.8%;         Pred. No. 1.5e-258;           Matches 1073;         Conservative         0;         Mismatches         2;         Indels         0;         Gaps         0;           Qy         1         CGCGGGAGAGGCCATGGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGC
GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: March 4, 2005, 22:14:12; Search time 4246.77 Seconds (without alignments) 9859.425 Million cell updates/sec Title: US-10-040-647-5 Perfect score: 1100 Sequence: 1 CGCGGGACAGGACGCCATGGAAAAAAAAAAAAA	Minimum DB seq length: 0 Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	stl:* st2:* tc:* st3:* st4:* st5:* st5:* st5:* or equal	SUMMARIES Result Ouery No. Score Match Length DB ID Description	97.4 1077 3 CR590593 CR590593 (R590593 92.0 1014 3 CR605277 CR605277 R5.0 82.6 932 1 AL578261 AL578261 AL55870	669.8 66.9 743.6 CB529999 CB529999 624.8 56.8 633.1 AI126185 AI126185 AI126185 569.2 51.7 705.4 BM019026 AI1289.9 1219.4 BM053333 BM553333 525.8 47.8 591.1 AA161187 AA161187 548.8 47.7 824.4 AB018961 BM018961 BM018961 BM018961	500.6 45.5 825 4 B1257649 BIST7649 B18751057 4964.8 42.3 479 1 AA448095 AA448095 B17347 B1737649 B1727649 B1727649 B1727649 B1727649 B1727649 B1727649 B0717268 B0717268 B0717268 B0717368 B0717368 B0717368 B0717368 B0717347 B0717

엄 ò 유 ò 쉱 à g ò

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
full-length cDNA clone CSODK002YM07 of HeLa cells Cot 25-normalized of Homo sapiens (human).
CR605277
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (Dases 1 to 1014)
1. i., W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGACTCAGGAAGCCGGAGTCGCAGGAGGGGGCGCCGTTATCAGGACCATGCGGCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGAC
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                                                                                                                                                                                                                                                            Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="kexon:9606"
/tb_me="CSDEXODYMO7"
/tissue type="Hela cells Cot 25-normalized"
/plasmid="pcMvSPORT_6"
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Pred. No. 1.3e-243;
0; Mismatches 1;
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                                                           CR605277.1 GI:50486084
HTC; CNSLT CDNA.
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Best Local Similarity 99.9%;
Matches 1013; Conservative
                                                                                  HTC; CNSLT CDNA.
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/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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al Similarity 98.6%;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31316478.
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AL578261 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODKO02XM07 3-PRIME, mRNA sequence.
                                                                                                541 GGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCCACACCCTCCAGGAAGTTCAGG
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                   TCTGTCTCCAGGCCTCCACATTTGAGAACCGGACAGACTGCTGGGTGACTGGCT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

13. (Dases 1 to 1057)

24. (Dases 1 to 1057)

25. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

26. Full-length cDNA libraries and normalization

27. In May 13, 2003 this sequence version replaced gi:30654423.

28. Contact: Genoscope

28. The Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

29. The Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: secref@genoscope.cns.fr. Web: www.genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCWVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Intitrogen.
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BX417595 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE010YP05
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BX417595 EXIME, MENA sequence.
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                                                                                                      362 TACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCC
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For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODE010CH03QP1&c=8290.f.

Location/Qualifiers
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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1. (bases 1 to 884)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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   AL555870.3 GI:45860593
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Matches 882; Conservative
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr web
ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 8290.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAKO26CBOINM1&c=8290.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone="CSDBE010YPOS"
/tissue_type="PLACENTA"
/tissue_type="PLACENTA"
/clone_lib="Homo aspiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                  BX454526 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YP05 3-PRIME, mRNA sequence.
 Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 CT-GGGCACTCACGGCGG-CGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCC
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Pred. No. 2.8e-185;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 898)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
                                                                                                         987
                                                                                                                                           981
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                                                                                                                              954 TGAGCTWACTGAGCCWATGCASCTGGGG
                                                                                                         960 GAGCCTACCTGAGCCCATGCAGCCTGGG
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BX454526.1 GI:31019139
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Best Local Similarity 96.5%;
Matches 862; Conservative
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           /clone="CSODEGIOYPOS"
/tissue type="PLACENTA"
/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                              23; Indels
                                                                                                                                                                                           78.7%; Score 866; DB 5; L 95.3%; Pred. No. 9.4e-207; tive 13; Mismatches 23;
xref="taxon:9606"
                                                                                                                                                                                                             Best Local Similarity 95.3% Matches 942; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B. NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayaed by: Incyte Genomics, Inc.

CDNA Library Arrayaed by: Incyte Genomics, Inc.

CLONG distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

Http://image.llnl.gov

Plate: LiAMN1343 row: h column: 06

High quality sequence stop: 826.
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871 bp mRNA linear EST 30-JUL-2001
602997320F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5139509 5',
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878 bp mRNA linear EST 04-OCT-2001
60303575F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5165562 5',
B1827608
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="twace:5165562"
/tissue_type="medulla"
/lab_host="DH108"
/clone_lib="NH1 MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon
                                  361 ATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGT 420
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
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                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procuremen: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The IM.A.G.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov e column: 19
Plate: LLAM1411 row: e column: 19
High quality sequence stop: 828.
I. .878
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Homo sapiens
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                                                                                                                                                                                                             BI259237 17-JUL-2001 777 bp mRNA linear EST 17-JUL-2001 602970095F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109695 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.MA.G.B. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 777.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 777)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                              1025 GTTTGGTAATAAACACATTC 1044
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CB529999 743 bp mRNA linear EST 05-AUG-2004 UI-H-FT2-bji-b-24-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone UI-H-FT2-bji-b-24-0-UI 3', mRNA sequence.
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Best Local Similarity 94.1
Matches 723; Conservative
   868 GGCTCTTCCA 877
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cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."
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                                                                                                                                                        38; Gaps
                                                                                                                     66.7%; Score 733.6; DB 4; Length 878; 93.7%; Pred. No. 1.9e-173; ive 0; Mismatches 19; Indels 38
                                                                                                                                      Best Local Similarity 93.73
Matches 853; Conservative
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                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/cgap.html
POLYA=Yes.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea to 70%) Primates; Catarrhini; Hominidae; Homo. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/note="Vector: pr7730-Pac"(Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                            Sequencing Center
information can be
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Pred. No. 4.3e-146;
0; Mismatches 4; Indels 0
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Ph.D.,
                                           CONSTITUTION Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 912 Std Brror: 0.00
Seq primer: -40013 fwd. ET from Amersham
High quality sequence stop: 455.
  Bento Soares,
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1735929"
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NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
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cloned into EcoRI/XhoI sites using the following §' adaptor: GGCACGAG(G). Library constructed by Ling Hoi in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH_MGC Library."
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/note="Organ: brain; Vector: pcMV-SPORT6; Site 1: NotI;
/note="Organ: brain; Vector site is a liso-dr primed and anonymous male age 27. Library is oliso-dr primed and directionally cloned (EcoW site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lefound through lah. I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov
Plate: LLAM12761 row: o column: 23
High quality sequence stop: 553.
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91.8%; Pred. No. 6.5e-127;
ive 0; Mismatches 52; Indels 2;
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                                                                                      AA161187 16-DEC-1996 2o59b06.sl Stratagene pancreas (#937208) Homo sapiens CDNA clone IMAGE:591155 3' similar to TR:E218488 E218488 TRYPTASE ;, mRNA
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1 (bases 1 to 591)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hulkman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 386.
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                                                                                                                                                                                  AA161187.1 GI:1735441
                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                           DEFINITION
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                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
MEDLINE
PUBMED
COMMENT
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                                                      RESULT 15
                                                                                                                                                                                                                                                                                                            AUTHORS
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410 TCTTTGGAGACATGGTTTGTGCTGGCAAATGCCCAAGGCGGGAAGGATGCCTGCTTCGGT 351
                                                                                                                                                                                                                                                                         290 AGCTGGGGAGTGGGGCTGTGGGNTCGCCCAATCGGCCCGGTGTCTACACCCAATATCAGCCAC
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Sequence Sequence Sequence Sequence

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Run on:

Scoring table:

Searched:

Minimum | Maximum |

Database

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Sequence 5, Application US/10040647

Sequence 5, Application US/10040647

Publication No. US20030092154A1

GENERAL INFORMATION:

APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David

TITLE OF INVENTION: NOVEL MOLECULES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE SONDESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

CLIY: GARDEN CITY

STATE: NEW YORK

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATHS:
FILING DATE: 07-Jan-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/023,942
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: PF0422/97
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: PP0422/97
FILING DATE: 13-FEB-1998
APPLICATION NUMBER: INTERNATION:
RILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
US-09-906-838-256
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       US-10-040-647-5
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     Sequence 5, Appli
Sequence 256, App
                                                                                                                     2005, 04:37:53 ; Search time 722.188 Seconds (without alignments) 9038.138 Million cell updates/sec
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                                                                                                                                                                                                        Description
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-909-120-256

US-09-909-08BB-256

US-09-902-853-256

US-09-907-841-256

US-09-907-841-256

US-09-904-011-256

US-09-908-03-640-256

US-09-908-03-256

US-09-908-03-256

US-09-908-03-256
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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DB seq length: 200000000
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1090.6 1090.6 1090.6 1090.6 1090.6 1090.6

Score

Result No.

900 900

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TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR PAPITCATION NUMBER: PCT/USO/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
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CURRENT FILING DATE: 2002-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 256, Application US/09909320 Patent No. US20020132240A1
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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100.0%; Score 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
                  REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEPX: (516) 742 4366
TELEX: 230 901 SANS UR
                                                                                                                                                                                                                                                                                                                     LOCATION: 17..961
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                   INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DA
    FRANK S
    NAME: DIGIGLIO,
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17..
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            544 CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCA 603
                                                                                  GGTCGCCATCATAAACAACTCTATGTGCAACCCCCTCTTCCTCAAGTACAGTTTCCGCAA
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 256, Application US/0990908BB
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT Genentech, Inc.
APPLICANT Botestein, David
APPLICANT Batcon, Dan L.
APPLICANT Batcon, Dan L.
APPLICANT Ferrara, Napoleone
APPLICANT FIVaroff, Ellen
APPLICANT FIVaroff, Ellen
APPLICANT Gerber, Hanspeter
APPLICANT Gerber, Hanspeter
APPLICANT Gerber, Hanspeter
APPLICANT Gerter, Mary E.
APPLICANT Goddard, A.
APPLICANT: Goddard, A.
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Pred. No. 0;
0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-01-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-30

PRIOR PLING DATE: 1999-12-30

PRIOR PLING DATE: 1999-12-30

PRIOR PLING DATE: 1999-12-30
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Best Local Similarity 99.6%;
Matches 1093; Conservative
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; ORGANISM: Homo Sapien
US-09-909-320-256
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961 AGCCTACCTGAGCCCATGCAGCCTGGGGACTCTGCGAAGTCAGGCCCTGGTTCTCTTCTG 1020
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                                             484 CATCTGTCTCCCAGGCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG
                                                                                                                                                                                                           CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCA
                                                                                                                                                                                                                                              544 CTGGGGGTACATCAAAGAAGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCA
                                                                                                                                                                                                                                                                                                                                                     604 GGTCGCCATCATAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA
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Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Grimaldi, Christopher J.
Gurney, Austin D.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Geritsen, Mary E.
Goddard, A.
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larity 99.6%; Pred. No. 0;
Conservative 0; Mismatches
PRIOR FILING DATE: 1001-07-13

PRIOR FILING DATE: 2000-02-2

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR PELLING DATE: 1999-07-28

PRIOR PELLING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PELLING DATE: 1999-09-13

PRIOR PELLING DATE: 1999-09-13

PRIOR PELLING DATE: 1999-09-13

PRIOR PELLING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/213089

PRIOR PELLOR DATE: 1999-09-15

PRIOR PELLOR DATE: 1999-11-29

PRIOR PELLOR DATE: 1999-11-29

PRIOR PELLOR DATE: 1999-11-29

PRIOR PELLOR PELLOR NUMBER: PCT/US99/28313

PRIOR PELLOR DATE: 1999-11-29

PRIOR PELLOR DATE: 1999-11-29

PRIOR PELLOR DATE: 1999-12-00

PRIOR PELLOR DATE: 1999-12-00

PRIOR PELLOR DATE: 1999-12-00

PRIOR PELLOR DATE: 1999-12-00

PRIOR PELLING DATE: 1999-12-00
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; ORGANISM: Homo Sapien
US-09-909-088B-256
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Best Local Similarity
Matches 1093; Conserv
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CTGGGCACTCACGGCGCGCCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG
                                                                                                                                                                                                CTACACCCGTTACTTCGTATCGAATATCTTGAGCCCTCGCTACCTGGGGAATTCACC
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Publication No. US2002019265941
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.;
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Bestow, Dan L.
APPLICANT: Faton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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US-09-902-853-256
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                        APPLICANT: Roy, Magrate Ann
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REPERRENC: 10466-14
CURRENT APPLICATION WORBER: US/09/09.291A
CURRENT PILING DATE: 2001-07-12
PRIOR PELING DATE: 3000-07-22
PRIOR PELING DATE: 3000-07-22
PRIOR PELING DATE: 3000-07-22
PRIOR PELING DATE: 3000-07-23
PRIOR PELING DATE: 1099-07-08
PRIOR PELING DATE: 1099-07-08
PRIOR PELING DATE: 1099-07-08
PRIOR PELING DATE: 1099-07-18
PRIOR PELING DATE: 1099-07-18
PRIOR PELING DATE: 1099-07-18
PRIOR PELING DATE: 1099-10-18
PRIOR PELING DATE: 1099-10-19
PRIOR PELING DATE: 1099-10-19
PRIOR PELING DATE: 1099-11-20
PRIOR PELING DATE: 1090-11-20
PRIOR PELIN
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; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.6%;
Matches 1093; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-291A-256
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961 AGCCTACCTGAGCCCATGCAGCCTGGCCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTG 1020
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                                                                                          GTGGATGGTCCAGTTTGGCCAGCTGCTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA 360
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                                                                                                                                                                   PRICANT: KIJa..
PRICANT: MATCHER, James

PRELICANT: PROMINE KIJa..
PRILICANT: PROMINI, Micholas F.
PRELICANT: PROMINI, Micholas F.
PRELICANT: PROMINI, Micholas F.
PRELICANT: Timochy A.
PRELICANT: Timochy A.
PRELICANT: Timochy Milliami, P. Micchy
APPLICANT: Williams, P. Micchy
APPLICANT: Wold Williami, P. Micchy
APPLICANTON NUMBER: US/09/902,853
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT PELICATION NUMBER: US/09/902,853
CURRENT PELICATION NUMBER: US/09/9065,300
PRIOR PLILICATION NUMBER: US/09/9065,300
PRIOR PLILICATION NUMBER: PCT/US99/20094
PRIOR PLILICATION NUMBER: PCT/US99/20094
PRIOR PLILICATION NUMBER: PCT/US99/20094
PRIOR PLILICATION NUMBER: PCT/US99/20094
PRIOR PLILICATION NUMBER: PCT/US99/20091
PRIOR PLILICATION NUMBER: PCT/US99/20099
PRIOR
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Pred. No. 0;
0; Mismatches
                                                                               Goddard, A.
Godowski, Paul J.
Godowski, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                  Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 99.6%;
Matches 1093; Conservative
                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGGCACTCACGCCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCCCCCACACCTCCAGGAAGTTCA 603
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                                                                                                                                                                                                                                                                                                                                                    Length 1100
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                                                                                                                                                                       Score 1090.6;
Pred. No. 0;
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                                                                                                                                                                       99.14;
                                                                                                                                                                   Query Match
Best Local Similarity 99.6
Matches 1093; Conservative
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-256
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APPLICANT: Pani, Nicholas F.
APPLICANT: Scewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Walliam, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20544
PRIOR PLING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-110-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR PRIOR DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1990-01-05
PRIOR PILING DATE: 1990-12-00
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
                               Sequence 256, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: ABARenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                   Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wei-Oiang
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APPLICANT:
APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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US-09-907-841-256
; Sequence 256, Application US/08907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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APPLICANT: Ashkenzi, Avi
APPLICANT: Bottein, David
APPLICANT: Beton, Duc
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ORGANISM: Homo Sapien
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Score 1090.6;
Pred. No. 0;
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Query Match
Best Local Similarity 99.6%;
Matches 1093; Conservative
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64 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGGCGCCG 123
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Pred. No. 0;
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Best Local Similarity 99.6
Matches 1093; Conservative
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; ORGANISM: Homo Sapien
US-09-904-011-256
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FRIOR FILING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-08
FRIOR FILING DATE: 1999-07-08
FRIOR FILING DATE: 1999-07-08
FRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-110-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/28564
FILLING DATE: 1999-12-02
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US-09-904-011-256
; Sequence 256, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.; APPLICANT: Ashkenazi, Avi
; APPLICANT: Bostorin, David
; APPLICANT: Besnoyers, Luc
; APPLICANT: Besnoyers, Luc
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Gerritsen, Mary E.
Goddard, A.
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Gao, Wei-Qiang
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botsovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goo, Wei-Qiang
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                                                                                                                                                         DB 10; Length 1100;
                                                                                                                                                                                                     4; Indels
                                                                                                                                                     Score 1090.6; Pred. No. 0; 0; Mismatches
                                                                                                                                                       99.1%;
ilarity 99.6%;
Conservative
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 256
; LENGTH: 1100
; TYPE: DNA
; ORGANIEM: Homo Sapien
US-09-908-093-256
                                                                                                                                                       Query Match
Best Local Similarity
Matches 1093; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mather, Johnson P. APPLICANT: Mather, Johnson P. APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Williams, P. Mickey APPLICANT: Wood, Williams, P. Mickey APPLICANT: Wood, Williams, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE REFERENCE: 10460-14
CURRENT PELLING DATE: 2001-07-17
PRIOR PELLING DATE: 2001-07-17
PRIOR PILLING DATE: 2001-07-17
PRIOR PELLING DATE: 2000-09-18
PRIOR PILLING DATE: 2000-09-18
PRIOR PILLING DATE: 2000-02-22
PRIOR PELLING DATE: 1090-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-09-18
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-00-15
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/30095
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
                                      RESULT 10
US-09-908-093-256
; Sequence 256, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                       Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                            Gerritsen, Mary E
                                                                                                                                                APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGGACGCCCGAACTCGGGCGTTGGCCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1090.6;
Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30565
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 256
FEMALTH 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6'
Matches 1093; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT APPLICATION NUMBER: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-09-18
PRIOR PLILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-28
          904 CTCCTGGCCACTACTCTTTTCCCTCTTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG 963
                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
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PILING DATE: 1999-10-05
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 256, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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Gao, Wei-Qiang
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/28114
PRIOR APPLICATION NUMBER: PCT/US99/28114
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1990-12-20
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PRIOR PLILING DATE: 2000-01-05
PRIOR PLILING DATE: 2000-01-05
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CORGANISM: Homo Sapien
US-09-906-838-256
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Matches 1093;
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APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
                                                                                                                            784 CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACACAATATCAG
                                                                                                                                                                                                                                                                       CTCCTGGCCGCTACTCTTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG
                                                                             CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCCGGTGTCTACACAATATCAG
                                                                                                                                                                           CORRENT FILING DATE: 2001-07-15
PRIOR PELING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-02-2
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 256, Application US/09906838 Publication No. US20030027143A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Clang
Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
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Eaton, Dan L.
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121 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGGACGCCCGAACTCGGGCGTTGGCCGTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC 420
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Pred. No. 0;
0; Mismatches
                    FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%;
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Best Local Similarity 99.6
Matches 1093; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM:
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 CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCA
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                                                                   GGTCGCCCATCATAAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAAGTTTCCGCAA
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF: INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 256, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Ferrara, Napoleone
Filvaroff, Ellen
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Hillan, Kenneth, J
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Paoni, Nich
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APPLICANT: Wood, William, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same Pile Reperence: 10466-14

CURRENT PILING DATE: 2002-01-22

FRIOR FILING DATE: 2000-02-2

FRIOR PELICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-14

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-11-05

PRIOR PELING DATE: 1999-11-05

PRIOR PELING DATE: 1999-11-05

PRIOR PELING DATE: 1999-11-05

PRIOR PELING DATE: 1999-12-07

PRIOR PELING DATE: 1999-12-05

PRIOR PELING DATE: 1999-12
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99.6%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                      Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Best Local Similarity 99.6
Matches 1093; Conservative
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; ORGANISM: Homo Sapien
US-09-907-942-256
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenzi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Eaton, Dan L.
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APPLICANT: Stewart, vimcury A.
APPLICANT: Tunnas, Daniel
APPLICANT: Tunnas, Daniel
APPLICANT: Williama, P. Mickey
APPLICANT: Wood, Milliama, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
GURREAT APPLICATION SECRETE and Sold of Sold of
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99.1%; Score 1090.6;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1093; Conservative 0; Mismatches
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
Rooni, Nicholas F.
Roy, Margaret Ann
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            Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
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Publication No. US20030036060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.;
APPLICANT: Ashkenazi, Avi
APPLICANT: Desnoyers, Luc;
APPLICANT: Baton, David
APPLICANT: Baton, David
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qa		Db 1084 AAAAAAAAAAAAAA 1100
, 9 9	61 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCG 120 	Search completed: March 5, 2005, 15:38:10 Job time : 727.188 secs
λο q	121 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGGGCCGAACTCGGGCGTTTGGCCGTG 180	
<u>ک</u> و	181 GCAGGGAAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG 240	
රු සි	241 CTGGGCACTCACGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300	
<u></u> ይ	301 GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA 360	
کو م م	361 CTACACCGTTACTTCGTATCGAATATCTGAGCCCTCGCTACCTGGGGAATTCACC 420 	
දු දු	421 CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGCACTACACTAACACATCCAGCC 480	
රු පු	481 CATCTGTCTCCAGGCCTCCACATTTGAGTTTGAGAACGGGACAGACTGGCTGG	
& 8 8	541 CTGGGGGTACATCAAAGAGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCA 600	
දු දු	601 GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA 660 	
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රු සි	721 CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGTGGTTGAGGT 780 	
ò a	781 CGTGAGCTGGGGGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATA†CAG 840 	
රු අ	841 CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAGAGTGGCATGTCCCAGCCAG	
& g	901 CTCCTGGCCGCTACTCTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG 960	
දු යු	961 AGCCTACCTGAGCCCATGCCACTGGGGACTAGGCCAAGTCAGGCCCTGGTTCTTCTG 1020	
% q	1021 TCTTGTTTGGTAATAACACATTCCAGTTGATGCCTTGCAGGCATTTTTCAAAAAAAA	
ò	1081 AAAAAAAAAAAAAA 1097 	

(otqsu) Anole Blank (uspto)

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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRICA PELICATION NUMBER: US/09/023,942A
FILING DATE: 13-FBE-1998
CLASSIFICATION DATA:
APPLICATION WUMBER: PO5101/97
FILING DATE: 11-FEB-1997
PRICA PAPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRICA DATE: 13-FBE-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELEPHONE: (516) 742 4343
TELEPHONE: (516) 742 4343
TELEPHONE: (516) 742 4343
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEOURCE CHARRATERSICS:
LENGTH: 1100 Dase pairs
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STRANDEDNESS: single
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                                                                                                                                               March 4, 2005, 22:18:30; Search time 205.888 Seconds (without alignments) 8742.154 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                       Description
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
Gencore version 5.1.6
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US-09-905-125A-256
US-09-905-175A-256
US-09-906-700-255
US-09-904-900A-256
US-09-904-900A-256
US-09-904-90A-256
US-09-906-618-256
US-09-908-21A-15
US-09-908-20-312D-431
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US-09-907-754A-262
US-09-907-754A-262
US-09-907-754A-262
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US-09-904-920A-262
US-09-909-064-262
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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5212, Ap
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Sequence 5, Application US/09023942A;
Patent No. 6479274;
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David;
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
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US-09-949-016-5210
US-09-949-016-5212
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US-09-98-016-36A-14
US-09-016-36A-14
US-08-978-404B-20
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961 AGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTG 1020
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                       Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoni, Nicholas F.
Roy, Margaret Ann
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Gao, Wei-Qiang
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                                          Score 1100; DB 4;
Pred. No. 6.5e-295;
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                                         Query Match
Best Local Similarity
Matches 1100; Conserv
LOCATION:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR PELING DATE: 2001-07-17
PRIOR PELING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21044
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28114
PRIOR APPLICATION NUMBER: PCT/US99/28114
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
1021 TCTTGTTTGGTAATAAACACATTCCAGTTGATGCCTTGCAGGGCATTTTTCAAAAAAA
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APPLICANT: FILVANCIF, ELIEN
APPLICANT: FONG, Sherman
APPLICANT: Gacy, Sherman
APPLICANT: Gacy, Sherman
APPLICANT: Gacy, Sherman
APPLICANT: Gacy, Wei-Ciang
APPLICANT: Goddard, A.
APPLICANT: Goddard, A.
APPLICANT: Goddard, P.
APPLICANT: Grimald, Christopher J.
APPLICANT: Giner, Austin J.
APPLICANT: Milan, Kenneth, J.
APPLICANT: Milan, Kenneth, J.
APPLICANT: Milan, Micholas F.
APPLICANT: Mather, Jenne P.
APPLICANT: Mather, Jenne P.
APPLICANT: Milan, Secreted and Transmembrane Polypeptides and Nucleic
APPLICANT: Millian, P. Mickey
APPLICANT: Millian, P. Mickey
APPLICANT: Millian, Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 11646-14
CURRENT PLILIGY DATE: 2000-02-22
FILE REPERENCE: 11999-07-07
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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                                                CICCIGGCCGCTACTCTTTTCCCCTCTTCTCGGCCTCTCCCACTCCTGGGGCCGGTCTG 960
                        Sequence 256, Application US/09905125A
Fatent NO. 6664376
GENERAL INFORMATION
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Bilen
APPLICANT: Food, Sherman
APPLICANT: Food, Sherman
APPLICANT: Gerber, Hangbeter
APPLICANT: Godowski, Paul J.
APPLICANT: Gedowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
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Pred. No. 2.7e-292;
0; Mismatches 4; Indels 0;
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 256
LENGTH: 1100
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.6
Matches 1093; Conservative
                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-794A-256
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembran;
TITLE OF INVENTION: Acids Encoding the Same;
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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Grimaldi, Christopher J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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APPLICANT: Genemicsch, Inc.
APPLICANT: Ashkenazi, Avii
APPLICANT: Botstein, David
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Eaton, Dan L.
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Pred. No. 2.7e-292;
0; Mismatches 4;
           PRIOR FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/23089
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Best Local Similarity 99.6
Matches 1093; Conservative
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CRGANISM: Homo Sapien
US-09-905-125A-256
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                                                                                                                                             GGTCGCCATCATAAACAACTCTATGTGCAACCACTCTTCCTCAAGTACAGTTTCCGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 256, Application US/09906700 Patent No. 6723535 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAAAAAAAAAA 1097
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Jang
Gerber, Hangpeter
Gerritsen, Mary E.
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APPLICANT: Ashkenati, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
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Pred. No. 2.7e-292;
0; Mismatches 4;
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
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Best Local Similarity 99.6%;
Matches 1093; Conservative
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       304 GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA 363
                                                                            CTACACCCGTTACTTCGTATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC
                                                                                                                                                                    CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGCACCTACACTAAACACATCCAGCC
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                                                                                                                                                                                                                                                                                                                                                         CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCA
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Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.;
APPLICANT: Ashkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
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Filvaroff, Ellen
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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Pred. No. 2.7e-292;
0; Mismatches 4;
                                                                              FILE KEKEKEMEN: 1.0496.14

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PRIOR FILING DATE: 1999-07-26

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PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

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PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

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Matches 1093; Conservative
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CORGANISM: Homo Sapien
US-09-906-700-256
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; Sequence 256, Application US/09904920A
; Patent No. 6806352
; Patent No. 6806352
; APPLICANT: Genentech, Inc.
; APPLICANT: Abhkenazi, Avi
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                        APPLICANT: Mather, Janua, Ivar J.
APPLICANT: Mather, Janua, Ivar J.
APPLICANT: Mather, Janua P.
APPLICANT: Pan, Janea
Ban, Janea
APPLICANT: Pan, Vincholas P.
APPLICANT: Pan, Vincholas P.
APPLICANT: Stewart, Timorh Ban.
APPLICANT: Stewart, Timorh Ban.
APPLICANT: Road, William I.
APPLICANT: Wood, William I.
APPLICANT: ON UNMER: 1080-00-00-10-11
RIOR APPLICATION WOMBER: US 60/143,048
RROR FILING DATE: 1999-00-12
RROR FILING DATE: 1999-00-13
RROR PLICANTON WOMBER: PCT/US99/20594
RROR PLICANTON WOMBER: PCT/US99/2059
RROR APPLICATION WOMBER: PCT/US99/2059
RROR PLICATION WOMBER: PCT/US99/2059
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Pred. No. 2.7e-292;
0; Mismatches 4; Indels 0;
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Best Local Similarity 99.6%;
Matches 1093; Conservative 0
                  Kljavin, Ivar J.
Mather, Jennie P.
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CRGANISM: Homo Sapien
US-09-903-603A-256
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Goddard, A.
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APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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FILE REFERENCE: 10466-14
CURRENT PRILING DATE: 2001-07-18
PRIOR PILING DATE: 2000-07-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
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FILING DATE: 1999-110-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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FILING DATE: 1999-11-30
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
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FILING DATE: 1999-12-02
                                                                    US-09-909-064-256
; Sequence 256, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
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Grimaldi, Christopher J.
AAAAAAAAAAAAA 1100
                                                                                                                                               Genentech, Inc.
Ashkenazi, Avi
Buttein, David
Besnoyers, Iuc.
Eaton, Dan L.
Ferrara, Nan Deneneri Privaroff, Bilen
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E
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Mather, Jennie P.
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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 256
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-909-064-256
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US09/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo Sapien
US-09-905-381A-256
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT PLING DATE: 2000-02-22
PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-28
PRIOR PELICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
     904 CICCIGGCCACTACTCTTTTCCCTCTTCTCGGGCTCTCCCCACTCTGGGGCCCGGTCTG 963
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 256, Application US/09905381A Patent No. 6818746
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Geneticch, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA 360
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Pred. No. 2.7e-292;
0; Mismatches 4;
                 FRIOR APPLICATION NUMBER: PCT/US99/21547
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-00-15
FRIOR PILING DATE: 1999-10-05
FRIOR PILING DATE: 1999-11-29
FRIOR APPLICATION NUMBER: PCT/US99/28113
FRIOR PILING DATE: 1999-11-30
FRIOR PILING DATE: 1999-11-30
FRIOR PILING DATE: 1999-12-02
FRIOR APPLICATION NUMBER: PCT/US99/28565
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR FILING DATE: 1999-12-02
FRIOR PILING DATE: 1999-12-02
FRIOR APPLICATION NUMBER: PCT/US99/30910
FRIOR APPLICATION NUMBER: PCT/US99/30910
FRIOR PILING DATE: 1999-12-16
FRIOR FILING DATE: 1999-12-00
FRIOR FILING DATE: 1090-10-05
NUMBER OF SEQ ID NOS: 423
FRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
FRIOR FILING DATE: 1000-01-05
NUMBER OF SEQ ID NOS: 423
FRIOR FILING DATE: 1000-01-05
FRIOR FILING
FILING DATE: 1999-09-15
PLILING DATE: 1999-09-15
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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99.6%;
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Best Local Similarity 99.6
Matches 1093; Conservative
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CORGANISM: Homo Sapien
US-09-906-618-256
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT PILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1024 TCTTGTTTGGTAATAAACACATTCCAGTTGATGCCTTGCAGGGCATTCTTCAAAAAAA 1083
                                                                                                                                                                                                                          CTCCTGGCCGCTACTCTTTTTCCCTCTTCTGGGGTCTCCCCACTCCTGGGGCCGGTCTG 960
                             904 CTCCTGGCCACTACTCTTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG 963
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEFX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     98.0%;
                                                                                                     LENGTH: 1094 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                       Query Match 98.0
Best Local Similarity 99.5
Matches 1094; Conservative
                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 17..955
US-09-023-942A-3
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 GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTCCGCAA 660
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                     GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA
                                                                           664 GGACATCTTTGGAGACATGGTTTGTGCTGGCAACGCCCCAAGGCGGGGAAGGATGCCTGCTT
                                                                                                                      CGGTGACTCAGGTGGACCCTTTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGT
                                                                                                                                                 724 cegreacreageaccerregecergraacaagaaregacreregrareagarregagr
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                                                           GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGCGGGAAGGATGCCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVERTION: (US only) ANTALIS Toni Marie and HOOPER John David TITLE OF INVERTION: NOVEL MOLECULES NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSE: SCHI'IV - STRREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION ATA:
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 13-FEB-1997
FILING DATE: 13-FEB-1997
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY PLAZA STATE: NEW YORK COUNTRY: USA
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; Sequence 3, Application US/09023942A
; Patent No. 6479274
; PATENT INFORMATION:
; APPLICANT: (US only)
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                        61 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCCGTTATCAGGACCATGCGGGCCG
                                                                                                                                                                                                                                                                          61 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTTATCAGGACCATGCGGCCC
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                                                                                                                       301 GIGGATGGICCAGTITGGCCAGCTGACTICCATGCCATCCTTCTGGAGGCCTGCAGGCCTA
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                                                             Gaps
                                                             9
      Length 1094;
                                                          Indels
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Score 1078; DB 4;
Pred. No. 8.3e-289;
0; Mismatches 0;
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Gaps

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180

300

323

420 443

263

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AGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTTCTG 1020
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                                                                                                                                                                   Length 1081;
                                                                                                                   3; Indels
                                                                         DB 3;
                                                                      Score 1051.2; DB 3
Pred. No. 2.2e-281;
0; Mismatches 3;
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-008-271A-15
                                                                      Query Match
Best Local Similarity 99.7%;
Matches 1053; Conservative
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                            CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAG
                                                                                              CTCCTGGCCGCTACTCTTTTCCCTCTTCTCTGGGCTCTCCCCACTCCTGGGGCCGGTCTG
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Gorley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRICATION DATA:
APPLICATION DATA:
APPLICATION WIMBER: <UNKNOWN>
FILING DATE: <UNKNOWN>
FILING DATE: <UNKNOWN>
OFFILING DATE:
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REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
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Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
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TELEPHONE: 650-855-0555
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LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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CITY: Palo Alto
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CLONE: 789927
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COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
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                                                                                740 TTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGC
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| Sequence 25, Application US/09023942A
| Sequence 25, Application US/09023942A
| Parent No. 6479274
| Parent No. 6479274
| Parent No. 197271
| APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
| TITLE OF INVENTION: NOVEL MOLECULES
| TITLE OF INVENTION: NOVEL MOLECULES
| CORRESPONDENCE ADDRESS: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
| STREET: 400 GARDEN CITY PLAZA
| CITY: GARDEN CITY STATE: NEW YORK
| STATE: NEW YORK
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APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
IN THE TORNEY ABOUT NOTHING ABOUT NOTHING ABOUT NOTHING ABOUT NOTHING ABOUT NUMBER:
NAME:
NAME:
DIGIGLO, FRANK S
REGISTRATION NUMBER:
TELECOMMUNICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-FEB.1998
CLASSIFICATION: 435
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TELEFAX: (516) 742 4364
TELEEX: 230 901 SAMS UR
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: DNA
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US-09-023-942A-25
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Pred. No. 4.4e-198;
0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/09386642
Fatent No. 6420157
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O1. Jenson
APPLICANT: O1. Jenson
APPLICANT: O1. Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ONT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 1103
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Best Local Similarity 93.4%;
Matches 784; Conservative
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US-09-386-642-59
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APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
CORRESPONDENCE 30
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
CITY: GARDEN CITY
STATE: NEW YORK
COUNTY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EPOPPY disk
COMPUTER: EPOPPY disk
COMPUTER: EPOPPY disk
COMPUTER: EPOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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LENGTH: 3866 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 357; Conservative
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                              Local Similarity 71.3%; Pred. No. 1.5e-123; nes 672; Conservative 0; Mismatches 253;
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3455 1456 ACCAATATCAGCCACCACCACTTGAGTGGATCCAGAAGCTGATGGCCCAGAGTGGCATGTCC 3515 1516 CAGCCAGACCCCTCCTGGCCGCTACTTTTTCCCTCTTCTCTGGGCTCTCCCACTCTCTG 3575 ö 3576 GGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTG 3635 769 830 ACCAATATCAGCCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAGAGTGGCATGTCC 889 CAGCCAGACCCCTCCTGGCCGCTACTCTTTTCCCTTCTCTGGGCTCTCCCACTCTCTG 949 710 GATGCCTGCTTCGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGTAT 3336 GCTGCTCCCCAGGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGAATGGACTGTGGTAT CAGATTGGAGTCGTGAGCTGGGGAGTGGCTGTGGTCGGCCCCAATCGGCCCGGTGTCTAC GGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGGCCACTGCCAAGTCAGGCCCTG Gaps ö Length 3866; Score 351.6; DB 4; Length Pred. No. 5.3e-87; 0; Mismatches 9; Indels 1010 3636 ò 8

RESULT 15
US-09-021-942A-27
Sequence 27, Application US/09023942A
Patent No. 6479274
; GENERAL INFORMATION:

1070 TCAAAA 1075 |||||| 3696 TCAAAA 3701 Q 40

Search completed: March 5, 2005, 09:20:35 Job time : 209.888 secs

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Aav59119 Nucleotid
Aax52259 Protein P
Aaf72417 Human PRO
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                                                                                                                                                              Description
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                          nucleic search, using sw model
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Maximum DB seq length: 2000000000
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						activity; viability; HELA2; ATC2; .880r; testicular germ cell cancer; on; antitumour; sperm development;										involved in regulating cell activity testis-specific protease HELA2 used for imour suppressor.	
9 ADA13145 9 ADA13360 9 ADA42013 9 ADA42863 10 ADA42863 10 ADB77782 110 ADC39764 110 ADC39764 110 ADC39457 110 ADC39457 110 ADC3948 110 ADC3948 110 ADC3948 110 ADC39698 110 ADC39698 110 ADC39698 110 ADD39061 110 ADD39061 110 ADD39363	Alignments	1100 BP.			long isoform of HELA2	regulation; cell activity; fertility; suppressor; test specific expression; antitu		Location/Qualifiers 17961 /*tag= a /product= "HELA2"			0085.	5101. 0422.	PTY LTD.				167pp; English.
99999111111000000000000000000000000000		standard; DNA;			sequence of 1	sin; stis		Location/ 17961 /*tag= a /product=			; 98WO-AU000085	; 97AU-00005101 ; 97AU-00000422	AD OPERATIONS	Hooper JD;	3-480768/41. Jaw77297.	serine protease(s) and kinase viability – particularly the Lation of fertility and as tu	62-64;
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661 GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGCGGGAAGGATGCCTGCTT 720
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        The present sequence represents the nucleotide sequence of the long isoform of HELA2. cDNA generated from HeLa cells and PAI-2 expressing HeLa cells was amplified using PCR primers AAV48312-13. Three new sequences were detected in the 480 bp amplicon. These sequences are designated HELA2 and ATC2 which have high homology to serine proteases and BCOM3 which has homology to a kinase. The proteins are involved in or associated with regulation of cell activity and/or viability.

Administration of recombinant HELA2 (also called testisin) is used to correspond in come non-testicular germ cell cancers (seminoma) and is also expressed in some non-testicular germ cell cancers (seminoma) and is also correspond in some non-testicular germ cell cancers (seminoma) and is also expressed in some non-testicular germ cell cancers (seminoma) and is also condovary), so is a marker/potential therapeutic target for cancer. The promoter from the HELA2 gene is useful for testis-specific expression of char genes, e.g. for gene therapy or modulation of fertility. Drugs that the block activity of HELA2 should have antitumour activity (other than in testis recombinant HELA2 should stop growth of tumours and normalise sperm development (ellminating the need for orchidectomy).
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Zollinger-Ellison syndrome; gastrointestinal ulceration;
congenital microvilus atrophy; skin disease; cell growth;
abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
                                                                                                                 CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCCAATCGGCCCCGGTGTCTACACCAATATCAG
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97US-0063542P.
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97US-006374P.
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24-0CT-1997;
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28-0CT-1997;
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28-0CT-1997;
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AAX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PR0211 and PR0217 can be used for disorders associated with the preservation and mintenance of gastrointestinal mucosa and the repair of acute and chronic encosal lesions (e.g. enterocolitis, 2011inger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including PR0265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PR0264 can be used as for fibromodulin, e.g. for reducing dermal carating and treatment of Usher Syndrome or Atrophia areata; PR0269 can be used an anti-thrombotic agent; PR0287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PR0317 can be used for treating problems of the kidney, uterus, endometrium, con be used for treating problems of the kidney, uterus, endometrium, but the place of the place of the kidney in the heart of genital tract 귱 New isolated human genes and polypeptides used in, e.g. treatment gastrointestinal ulceration. Yuan J; Chen J, Goddard A, Pennica D, Claim 2; Fig 91; 320pp; English. Gurney AL, WPI; 1999-229533/19.

Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;

1024 964 1021 상 원 Gaps Query Match
99.1%; Score 1090.6; DB 2; Length 1100;
Best Local Similarity 99.6%; Pred. No. 4.4e-227;
Matches 1093; Conservative 0; Mismatches 4; Indels 0;

1083

1080 AGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTCTTCTG 1023 240 120 123 183 243 300 303 360 363 420 423 480 483 540 543 600 603 9 663 720 723 780 783 843 900 903 960 963 63 GGCTGGACTCAGGAAGCCGGAGTCGAGGAGGCGGCGCCGTTATCAGGACCATGCGGCC GCAGGGGAGCCTGCGCCTGTGGGGATTCCCACGTATGCGGAGTGAGCCTGCTCCAGCCACCG CTGGGCACTCACGGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGCCCTA CATCTGTCTCCAGGCCTCCACATTTGAGTTTCAGAACCGGACAGACTGCTGGGTGAGCTGG AGCCTACCTAAGCCCATGCAGCCTCGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTG GGCTGGACTCAGGAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCG 121 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGGACGCCCGAACTCGGGCGTTGGCCGTG ACGGGTCATCACGTCGCGCATCGTGGGTGGAGGACGCCCGAACTCGGGCGTTGGCCGTG GCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG CTGGGCACTCACGGCGGCGCACTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACACAGCC CTGGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACCCTCCAGGAAGTTCA GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGT CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCATCGGCCCGGTGTCTACACCATATCAG CCACCACTITIGAGIGGATCCAGAAGCIGATGGCCCAGAGIGGCATGICCCAGCCAGACCC Grégarégrecagririséceaécréacrirecarécearecrireregaécerécaécera CTACACCGGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCC CATCTGTCTCCAGGCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCA GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCCAAGGCGGGAAGGATGCCTGCTT GGACATCTTTGGAGACATGGTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTTGCTT cereaecrececreresercecccarcescceserereracaccararacas ccaccactrigagingariccagaagcrgarggcccagagiggcargrccagccagaccc TCTTGTTTGGTAATAAACACATTCCAGTTGATGCCTTGCAGGGCATTTTTCAAAAAAA 61 124 184 244 364 424 544 64 181 241 301 304 421 481 484 541 601 604 661 664 721 724 781 784 841 844 901 904 196 361

us-10-040-647-5.rng

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The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynuclectides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Blison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarting and wound healing, nerve repair, thrombosis, bone and/or l cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclensis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature agging, ALDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; neuroprotective; vasotropic; chemotaxic; antivenentic; antivenentic; antiatheratics; antivenentic; antiatheratics; cardiant; antidiabetic; cerebroprotective; thrombolytic; immunomodulator; entercoclitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzhaimer's; ALS; neuropathy; dermal scarring; wound healing; esthma; rheumatorid arthritis; multiple sclerosis; inflammatory disorder; atherosclerosis; cardiac influry; infertility; premature aging; AlDS; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
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Conservative

Similarity

Best Local Sim: Matches 1093;

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Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                  Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antianglogenic; vasotropic; antiacthmatic; antirheumatic; cancer; antiarthitic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation; ss.
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1 ME, Goddard A;
Kljavin IJ;
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H, Gerritsen ME,
Hillan KJ, Klja
Stewart TA, Tur
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99US-0145698P.
99US-0146222P.
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P-PSDB; AAB80256.
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                      AAF72417 standard;
                                                                                   Human PRO303 cDNA
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The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, artherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping

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   Length 1100
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  DB 4;
Score 1090.6; DB 4
Pred. No. 4.4e-227;
0; Mismatches 4;
   99.18;
Query Match
Best Local Similarity 99.6
Matches 1093; Conservative
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polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing.
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10-SEP-1998;
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15-SEP-1999;
15-SEP-1999;
29-NOV-1999;
30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
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08-SEP-1999
TCTTGTTTGGTAATAAACACATTCCAGTTGATGCCTTGCAGGGCATTTTTCAAAAAAA 1080
                                Human; 88; gene; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker.
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Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen I
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, I
Mather UP, Pan J, Paoni NF, Roy MA, Stewart TA,
Williams PM, Wood WI,
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11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005811.
30-MAR-2000; 2000WO-US00581.
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97US-0066770P
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98WO-US018824
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Tumas D; New transmembrane polypeptides and nucleic acids encoding the WPI; 2003-329602/31.

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# Claim 2; Fig 91; 484pp; English.

The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of a secreted/transmembrane polypeptides, or RNO polypeptides or encoding a C RNO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO CC polypeptide (by culturing the host cell for the expression of the PRO CC polypeptide (No culturing the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (C an immino acid sequence selected from the 61 PRO proteins; (B) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of peptide), a chimaeric molecule comprising a PRO polypeptide of to a RNO polypeptide or to a PRO polypeptide of containing the polypeptide.

CC PRO1545 or PRO1868 in a sample suspected of containing the polypeptide, modulating at least one biological activity of a cell expressing a PRO245 or PRO1868 and containing at least one biological activity of a cell expressing a PRO245 or PRO1868 and containing at least one biological activity of a cell expressing a PRO245 or PRO1868 and containing the polyment either correct or PRO1868. Nucleic acids which encode PRO can be used to generate either

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Alzheimer's disease; inflammation; nephritis; wound healing;
nerve repair; collateral blood vessel formation; cancer;
colorectal cancer; haemorrhage; rheumatroid arthritis; diabetes;
cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
                                                                       CTCCTGGCCACTACTCTTTTTCCCTCTTCTCTGGGGTCTCCCCACTCCCTGGGGCCCGGTCTG
  Human; secreted and transmembrane protein; PRO; pharmaceutical;
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transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence encodes a PRO protein
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invention describes a new isolated nucleic acid molecule comprising

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970S-0063435P

970S-0063732P

970S-0063734P

970S-0063734P

970S-0063738P

970S-0064103P

970S-0064103P

970S-0064103P

970S-0064103P

970S-006480P

970S-006584E

970S-006584E

970S-006684E

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970S-00668E

970S-00668E
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98WO-US019330.
98WO-US019437.
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99WO-US020594.
99WO-US020944.
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2000WO-US005841.
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2000WO-US008439.
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                                                                                                                                         24-NOV-1997;
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## (GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-370793/35.

P-PSDB; ABO01818.

New genes and secreted and transmembrane polypeptides (e.g. PRO245 or RR0315), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia or strokes.

Claim 2; Fig 91; 482pp; English

the inventor and institute a new forecast and increase comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209289), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 164-1119 amino acids fully defined in the specification. The PRO polypeptides or polymucleotides are useful as comparent and defined in the specification. The PRO polypeptides or polymucleotides are useful as comparent and defined in the specification. The PRO polypeptides or polymucleotides are useful as comparent at defined in the second particularly useful for detecting or treating e.g. Parkinson's disease, allowed to a nation nearly ne 240 243 124 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTG 183 480 423 9 63 64 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCG 184 GCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGCCTA 544 CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACCCTCCAGGAAGTTCA 1 CGCGGGAGAGGCCATGGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTCG GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCG 241 CTGGGCACTCACGGCGCGCGCTTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG CTGGGCACTCACGGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC CTACACCCGTTACTTCGTATCCGAATATCTGAGCCCTCGCTACCTGGGGGAATTCACC CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCC 484 CATCIGICICCAGGCCICCACATITGAGITIGAGAACCGGACAGACIGCIGGGIGACTGG GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA 121 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGGACGCCGAACTCGGGCGTTGGCCGTG 181 GCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG 424 CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACACAGCC CATCTGTCTCCAGGCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCCACCACCTCCAGGAAGTTCA Gaps Query Match 99.1%; Score 1090.6; DB 8; Length 1100; Best Local Similarity 99.6%; Pred. No. 4.4e-227; Matches 1093; Conservative 0; Mismatches 4; Indels 0; Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other; 301 304 61 244 364 361 421 481 541 601 88888888888888888888888888888888 임 ð ò 셤 d g 셤 ò 원 셤 ð à ઠે 셤 ò ò 8 ò 요

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Eaton DL, Ferrara N;
Gerritsen ME, Goddard A;
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Fong S, Gao W, Gerber H,
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11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005641.
20-MAR-2000; 2000WO-US005641.
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14-SEP-1998;
16-SEP-1998;
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Filvaroff E,
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AGCCTACCTGAGCCCATGCAGCCTGCGCAAGTCAGGCCTGGTTCTTCTG 1020
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                    CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGGTATCAGATTGGAGT 780
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                                                                  CTCCTGGCCACTACTCTTTTTCCCTCTTCTCTGGGGCTCTCCCACTCCTGGGGCCGGTCTG
          GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGCGGGAAGGATGCCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; PRO; secreted protein; transmembrane protein; enterocolitis; gastrointestinal ulceration; skin disease; ss; gene; abnormal keratinocyte differentiation; psortasis; epithelial cancer; squamous cell carcinome; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; inflammatory disease; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; diabetic complication; wound repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA encoding secreted/transmembrane protein PRO303.
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Tumas D; Hillan KJ, Stewart TA, Å, Godowski PJ, Grimaldi JC, Gurney Mather JP, Pan J, Paoni NP, Roy Williams PM, Wood WI;

WPI; 2003-147434/14.

P-PSDB; ABU54391

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.

Claim 2; Fig 91; 473pp; English.

The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) any one of 61 fully defined amino acid sequence given in the specification (appearing as ABIG5437-catid sequences given in the specification (accession numbers of ABIG54407); (b) an amino acid sequence encoded by the nucleotide sequence deposited under Amarican Type Culture Collection (accession numbers of 11sted in the specification); (c) any one of the PRO sequences which can be people sequence sequences which is associated signal peptide; or (e) an one of the PRO polypeptide which lacks its associated signal peptide; or (e) an one of the PRO polypeptide which lacks its associated signal peptides. Vectors, host cells and anti-pRO antibodies. The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin disease associated with a sequence caids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin diseases associated with a sequence call carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory disease, e.g. theumatorid arthritis, asthma or multiple sclerosis, organ failure, atterosclerosis, cardiac injury, infertility, birth defects, premature adjing, AlbS cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating the propagentides, in assays to identify other proteins or molecules are also useful in the development and secening of therapeutically useful sequence, for complete and secured in the propagent and secured in man are useful in the development and secreming of therapeutically useful seagents, for chromosome identification, and cell suppose in binding reaction, to generate transgence animals or knockout animals, the reproduced assays for identify PRO polypeptide

Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;

ö 120 240 123 180 243 CTGGGCACTCACGGCGCGCCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 303 124 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGGACGCCCGAACTCGGGCGTTGGCCGTG 183 241 CTGGGCACTCACGGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300 9 63 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCG GCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCACCCC 1 CGCGGGAGAGGAGGCCATGGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTCGCTCG 4 ceceseasasasasccaresececececececececrecrecresecececres GGCTGGACTCAGGAGCCGGAGTCGCAGGAGCCGCCGCTTATCAGGACCATGCGGCCG ACGGGTCATCACGTCGCGCATCGTGGGTGGAGACGCCCGAACTCGGGCGTTGGCCGTG GCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG Query Match 99.1%; Score 1090.6; DB 8; Length 1100; Best Local Similarity 99.6%; Pred. No. 4.4e-227; Matches 1093; Conservative 0; Mismatches 4; Indels 0; Query Match 61 181 184 244

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964 AGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTCTTCTG 1023 480 483 900 603 099 663 720 780 783 840 963 GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTACAGGCCTA CTACACCCGTTACTTCGTATCTATCTGAGCCCTCGCTACTGGGGAATTCACCC GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA CGTGAGCTGGGGAGTGGGCTCGGCCCCAATCGGCCCCGGTGTCTACACCAATATCAG crargacarrecorrecterorecreterorecractaracacaracacarceagec CATCTGTCTCCAGGCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG CATCIGICACCAGGCCTCCACATITGAGTTTGAGAACCGGACAGACTGCTGGGGGACAGACTGG CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCA 664 GGACATCTTTGGAGACATGGTTTGTGCTGGCAACGCCCAAGGCGGGGAAGGATGCCTGCTT CGGTGACTCAGGTGGACCCTTGGCCTGTAACAATGGAATGGACTGTGGTATCAGATTGGAGT CTACACCCGTTACTTCGTATCGAATATCTGTGAGCCCTCGCTACCTGGGGAATTCACC CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACAAACACATCCAGCC credesegracarcaagagargageacrecearcreceacacecrecagaagrrea CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGT CGTGAGCTGGGGAGTGGGCTGTGGTCGCCCCAATCGGCCCGGTGTCTACACCAATATCAG 844 CCACCACTITGAGTGGATCCAGAAGCTGATGGCCCAGAGTGGCTATGTCCCAGACCC CTCCTGGCCGCTACTCTTTTCCCTCTTCTGGGCTCTCCCCACTCCTGGGGCCCGGTCTG GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGCGGGAAGGATGCCTGCTT 1081 AAAAAAAAAAAAA 1097 841 961 1021 304 361 364 421 481 484 541 544 604 661 721 724 784 904 301 424 601 781 901 RESULT 셤 ð 엄 ò 셤 à g 8 ద g 셤 g 8 ઠે ò à 셤 ò g ò 셤 ò g 셤 8 à

ACH06991 standard; cDNA; 1100 (first entry) 08-OCT-2003 ACH06991; 

BP

Human secreted/transmembrane polypeptide PRO303 cDNA.

Human; gene; ss; abnormal bleeding; gynaecological disease; asthma; hysterectomy; angiogenesis; coronary ischaemic condition; skin disease; gastrointestinal mucosa disorder; acute mucosal lesion; neuropathy; ALS; chronic mucosal lesion; abnormal kratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;

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uncontrolled cell growth, cancer; blood coagulation cascade; thrombosis; haemorrhage; endometrial bleeding; angiogenesis; wound healing; timour; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
                                                                                                        9705-0059115P
9705-0059117P
9705-0059117P
9705-0059114P
9705-0059121P
9705-0059124P
9705-0059124P
9705-0062287P
9705-0062287P
9705-0062314P
9705-0063124P
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98US-0104080P.
98US-0109304P.
                                                                                 10-JUL-2001; 2001US-00902903
                                                 US2003044839-A1.
                                  Homo sapiens.
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20-NOV-1998;
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c diagnosing or treating abnormal bleeding involved in gynecological diagnosing or treating abnormal bleeding involved in gynecological diagnosing or treating abnormal bleeding involved in gynecological diseases e.g. to avoid or lessen the need for hysterectomy. PR0317 may also be useful as an agent that affects angiogenesis and PR0317 is useful in anti-tumour indications or in treating occonary ischaemic conditions. PR0211 and PR0217 polypeptides are useful for treating disorders associated with the preservation and maintenance of gastrointestinal motors and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis). CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies and disease related to uncontrolled cell growth, e.g. cancer. PR0219 colypeptide plays a regulatory role in the blood coagulation cascade. PR0246 polypeptides which serves at tumour specific antigens may be exploited as therapeutic targets for anti-tumour drugs. PR026 polypeptides which serves at tumour specific antigens may be exploited as therapeutic targets for anti-tumour drugs. PR026 polypeptides and useful as an antithrombotic agent with reduced risk for haemorrhage as compared with heparin. PR0317 polypeptides and tissue repair. PR0234 polypeptides are useful for treating andometrial bleeding angiogenesis. PR0287 polypeptides and multiple sclerosis. The polypeptide and its nucleic acid are useful for tissue typing and/or assay of sample fluids. Anti-PR0 cantibodies are useful in diagnostic assay for PR0 e.g. detecting its cypression in specific cells, tissues or serum and for affinity

The invention relates to an isolated PRO polypeptide. PRO317 is useful in

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Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                Ferrara N;
en ME, Goddard A;
Kljavin IJ;
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                                                                                                                                                                                                 22-FEB-2000; 2000WO-US004414.

24-FEB-2000; 2000WO-US005004.

02-MAR-2000; 2000WO-US005841.

20-MAR-2000; 2000WO-US0057377.

30-MAR-2000; 2000WO-US00439.

22-MAY-2000; 2000WO-US014642.

22-UJN-2000; 2000WO-US01264.

28-JUL-2000; 2000WO-US012564.

24-AUG-2000; 2000WO-US012564.
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15-SEP-1999,
29-NOV-1999,
20-NOV-1999,
01-DEC-1999,
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AGCCTACCTGAGCCCATGCAGCCTGGGCCCACTGCCAAGTCAGGCCCTGGTTCTCTTGT 1020
                                                                                                                                                                                                                                                                                 Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical; diagnostic; biosensor; bioreactor; therapeutic; hyperplasia; endometriosis; cancer; tumour; ischaemia; coronary arterial disease; polycystic kidney disease; renal failure; inflammatory response; asthma; rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy; cytostatic; gynecological; cardiant; nephrotropic; hepatotropic; antiinflammatory.
                             AGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTG
                                                                                 rcrigiriggiaaraacacarrccagrigargccrigcagggarrcricaaaaaaaa
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                                                                                                                                                                GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCGTTATCAGGACCATGCGGCCG 120
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 present sequence represents cDNA encoding a human secreted/transmembrane PRO polypeptide
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                                                                                                                                                                               GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGAACATGCGGCCG
                                                                                                                                GCAGGGGAGCCTGCGCCTGTGGGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACC
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                                                                                             Gaps
                                                                   8; Length 1100;
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0
                                             Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;
                                                                                            4; Indels
                                                                  Score 1090.6; DB 8;
Pred. No. 4.4e-227;
0; Mismatches 4;
purification of PRO from recombinant
                                                                     99.1%;
99.6%;
                                                                                 Best Local Similarity 99.6
Matches 1093; Conservative
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### (GETH ) GENENTECH INC

Ferrara N; ME, Goddard A; Kljavin IJ; Tumas Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ellvaroff E, Fong S, Gao W, Gerbor H, Gerritsen Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Pan J, Paoni NF, Wood WI; Godowski PJ, Mather JP, Pa Williams PM,

#### WPI; 2003-288105/28. P-PSDB; ABU64543.

New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245) and genes encoding them, useful for detecting or treating e.g. hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease or inflammations.

# Claim 2; Fig 91; 477pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO protein solution polynucleotides are also useful as pharmaccuticals, diagnostics biosensors or bioreactors, for detecting or treating e.g. hyperplasis, endometriosis, cancers (e.g. those involving solid tumours), ischaemia,

844

ö coronary arterial disease, polycystic kidney disease, chronic or acute renal failure, or inflammatory responses (e.g. asthma, rheumatoid arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX96017-ABX96378 are the genes encoding, the primers amplifying and the probes detecting the PRO polynucleotides of the invention 120 180 240 300 360 420 480 540 543 900 99 720 780 840 123 243 303 363 423 483 603 663 723 783 900 124 ACGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCCGAACTCGGGCGTTGGCCGTG 183 9 63 CTGGGCACTCACGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA CATCTGTCTCCAGGCCTCCACATTGAGTTTGAGAACCGGACAGACTGCTGGGTGAGACTGG GGACATCTTTGGAGACATGGTTTGTGCTGGCAACGCCCAAGGGGGGAAGGATGCCTGCTT CGTGAGCTGGGGAGTGGGCTGTGGCTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAG cecesca Garaga Contra de Contra GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCG Gecrecacreacaaccecacrecacaccececececerrareacaaccarecece GCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG CTGGGCACTCACGCGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG GTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTA CTACACCCGTTACTTCGTATCGAATATCTGTGAGCCCTCGCTACCTGGGGAATTCACC CTACACCCGTTACTTCGTATCGAATATCTGAGCCCTCGCTACCTGGGGAATTCAC CTATGACATTGCCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCC CTATGACATTGCCTTGGTGAGCTGTCTGCAGCCTGTCACTAAAACACATCAGCC CATCTGTCTCCAGGCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGTGACTGG CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCCACACCCTCCAGGAAGTTCA CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCA GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGCGGGAAGGATGCCTGCTT CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGT CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGAATGGACTGTGGGTATCAGATTGGAGT CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAG Gaps Length 1100; ö Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other; 4; Indels DB 8; Query Match
99.1%; Score 1090.6; DB 8
Best Local Similarity 99.6%; Pred. No. 4.4e-227;
Matches 1093; Conservative 0; Mismatches 4; 4 61 64 121 181 184 241 244 301 304 484 541 544 604 661 664 721 724 781 841 361 364 421 424 181 601 784 8\$\$\$\$\$\$\$\$\$\$\$\$ ઠે 요 원 셤 g a 8 B 셤 ò ઠે 셤 8 8 셤 ઠે ઠે ద 8 ઠે 셤 ઠે ઠે 셤 ઠે g ò 8 à 셤

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Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245
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Kljavin IJ;
Tumas D;
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Hillan KJ, F
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20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US00414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005004.
         97US - 0063735P
97US - 0063738P
97US - 0063870P
97US - 0064208P
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97US - 0064208P
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         CTCCTGGCCGCTACTCTTTTTCCCTCTTCTGGGGTCTCCCCACTCCTGGGGGCGGTCTG 960
                        Human, gene therapy; mucosal lesion, ulcer; enterocolitis; skin disease; psoriasis; cancer; lung cancer; colon cancer; nerre cell disease; Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis; atrophia areata; inflammatory disease; asthma; rheumatorid arthritis;
                                                                      cDNA encoding human secreted protein PRO303.
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97US-0062814P
97US-0062814P
97US-0063121P
                                                                                                                                                                                                                                 ACA05549 standard; cDNA; 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-2001; 2001US-00906742
                                                                                                                                                                                                                                                                              29-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          ischaemia; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                      US2003023054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2003
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29-OCT-1997
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AGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTTGTG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cartilage;
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                                                                                                                                                                                                                                                                                                                  CICCIGECCACIACTCITITICCCTCTTCTCTGGGGCTCTCCCACTCCTGGGGCCGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                   AGCCTACCTGAGCCCATGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTG
                                                                                                                                                                             CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAG
                        GGACATCTTTGGAGACATGGTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTT
                                                                                          CGGTGACTCAGGTGGACCCTTGGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGT
                                                                                                                                       CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAG
                                                                                                                                                                                                                 CTCCTGGCCGCTACTCTTTTCCCTCTTCTCTGGGCTCTCCCCACTCCTGGGGCCGGTCTG
                                                            CGGTGACTCAGGTGGACCCTTTGGCCTGTAACAAGGATGGACTGTGGTATCAGATTGGAGT
  Human secreted / transmembrane polypeptide PRO303 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACD20216 standard; cDNA; 1100 BP
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970S - 0059184P
970S - 0059266P
970S - 0062125P
970S - 006228FP
970S - 006228FP
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97US-0059117P
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
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24-OCT-1997;
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                                                                                        The invention relates to sixty one nucleic acids encoding PRO
polypeptides (secreted and transmembrane). The polymucleotide is useful
in molecular biology, including uses as hybridisation probes, in
chromosome and gene mapping, in generating antisense RNA and DNA, and in
chromosome and gene mapping, in generating antisense RNA and in
considerably. The polymucleotide may also be used in preparing PRO
colypeptides by recombinant techniques, and in generating either
transgenic animals or knock-out animals which, in turn, are useful in the
development and screening of therapeutically useful reagents. The PRO
polypeptide or the antibody is used in preparing a medicament for
treating a condition reappositive to the polypeptide or antibody, such as
mucosal lesions e.g. ung cancer and colon cancer, nerve cell disease
comesal, sancer e.g. lung cancer and colon cancer, nerve cell disease
comesal, antipogenesis, inflammatory disease e.g asthma and
rhounatoid architis, ischaemia, and in various diagnostic assays. The
present sequence represents an CDNA which encodes a PRO polypeptide
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or {\tt PRO1868}, useful in chromosome and gene mapping, in generating , antisense RNA and DNA, and in treating cancer and Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;
                                                            Example 41; Fig 91; 481pp; English
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The invention relates to an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide. The polypeptide is useful for identifying agonists or antegonists of the polypeptide, for preparing variants of the polypeptide, as molecular weight markers for protein clertrophoresis purpose and the nucleic acid is useful for recombinantly expressing those markers. The polypeptide is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The nucleic acid is useful as therapeutic acid is useful as therapeutic or hybridisation probes, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation pobes for mapping the gene which encodes the PRO and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes for polymerase chain reaction (PCR), Northern analysis, Southern analysis and Western analysis. PRO antibody is useful for the passays for PRO, e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The polypeptide or its antibody e.g. tumour. The polypeptide and the nucleic acid is useful for treating obseit, or hypo- or hyper-insulinaemia and cardiac insulficiency disorders, for inducing regeneration of additory hair cells and for reacting bearing loss in mammals and for treating bone and/or cartilage disorders such as sports injuries and arthritis. The presents sequence crepresents conding a human secreted and transmembrane PRO polypeptide. 61 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGCCGCCGCTTATCAGGACCATGCGGCCG 120 121 ACCCCTCATCACCTCCCCCATCCTCGTCGACACGCCCCAACTCCGGCCGTTGGCCCGTG 180 Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers. 64 GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCG 124 Acedentarchicercecarceregeregaedececeaacregecere 181 GCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTGCTCAGCCACCG Gaps Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI; 99.1%; Score 1090.6; DB 8; Length 1100; 99.6%; Pred. No. 4.4e-227; ive 0; Mismatches 4; Indels 0; Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other; Claim 2; Fig 91; 469pp; English. 18-SEP-2000; 2000US-00665350. Matches 1093; Conservative (GETH ) GENENTECH INC. WPI; 2003-417923/39. Local Similarity P-PSDB; ABO14909 polypeptide Query Match Best 8 셤 ð à 셤 ò

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184 GCAGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACGG

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keratinocyte differentiation, epithelial cancer, Alzheimer's disease, squamous cell carcinoma, Parkinson's disease, inflammatory disease, amyotrophic lateral sclerosis, rheumatoid arthritis, asthma, multiple sclerosis, organ fallure, atherosclerosis, cardiac injury, infertility, birth defect, premature aging, AIDS, cancer; diabetic complication, wound repair, tissue re-growth; gene; ss.
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Amther JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-341586/32. P-PSDB; ABU69666.

ä New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.

Claim 2; Fig 91; 473pp; English.

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating entercolitis, gastrointestinal culeration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma. Alzheimer's disease, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with reconstructions or the PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein clertrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This sequence encodes a convenience of the con

Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;

. Query Match

99.1%; Score 1090.6; DB 8; Length 1100;

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The invention relates to an isolated secreted and transmembrane PRO polypeptide. The PRO polypeptides are useful for modulating biological activity of a cell, in diagnosing or treating abnormal bleeding involved
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16-DEC-1999; 99W0-US030095.
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25 - OCT - 1997;

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in gynaecological diseases e.g. to avoid or lessen the need for 'hysterectomy, for treating angiogenesis, tumour, coronary ischaemic condition, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal (differentiation) (e.g. psoriasis), Parkinson's disease, Alrheimer's disease, amyorrophic lateral solerosis (ALS), neuropathies, disease, amyorrophic lateral solerosis (ALS), neuropathies, disease, cascade disorders, neurodegenerative disease, thrombosis, haemorrhage, endometrial bleeding, wound healing, tissue repair, asthma, rheumatoid arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are useful in molecular biology including uses as hybridisation probes and in the generating transgenic animals or knockout animals. The PRO contibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for sample fluids. Anti-PRO antibodies are useful in diagnostic assays for sample fluids. Anti-PRO antibodies are useful in diagnostic assays for sample fluids. Anti-PRO antibodies are useful in diagnostic assays for sample fluids. The present sequence represents colls, tissues or serum and contrasting transmembrane PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;
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Matches 1093; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGAGCTGGGGAGTGGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAG
                                                                                                                                                    CTCCTGGCCGCTACTCTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG
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21-OCT-1997;
24-OCT-1997;
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CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCA 544 CTGGGGGTACATCAAAGAGGATGAGGCACTGCCATCTCCCCACACACCTCCAGGAAGTTCA GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA GGTCGCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAA GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCCAAGGCGGGAAGGATGCCTGCTT

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9705-0063120P-
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22-MAY-2000;
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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucled acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptides for linking a bloactive molecule to a call expressing a PRO polypeptides are useful for detecting other PRO polypeptides are useful for detecting other PRO polypeptides are useful for detecting other PRO polypeptides are useful for modulating the bological activity of a call expressing a PRO polypeptides are useful for modulating the bological activity of a call expressing a PRO polypeptides are also useful for detecting disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases, amyotrophic lateral sclerosis (ALS), menopating and maintenance of gastrointestinal sease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for lessening the effects of viral antithrombotic agent with reduced risk for hemorrhage as compared with cheparin, in treating other PRO-apporties can be also used in assays to determine if the have a role in naurodegenerative diseases or their reversal as an antithrombotic agent with reduced risk for hemorrhage as customerial bleeding angiogenesis, and may also have an effect on kidney to relate the full-length PRO-CDNA or to isolate the full-length pro-CDNA or to isolate other compared with the general propertied and gene mapping, in the generating transgenic and gene mapping, in the generating transgenic and gene ma Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher used in gene therapy, particularly for replacing a defective gene. The propertive gene. The propertion and the sective gene. The propertion and the sective gene. The propertion and the sective gene. The propertion and the section and the Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D; Claim 2; Fig 91; 469pp; English. 02-JUN-2000; 2000WO-US015264. 28-JUL-2000; 2000WO-US020110. 24-AUG-2000; 2000WO-US023328 18-SEP-2000; 2000US-00665350. Ashkenazi A, Botstein D Filvaroff B, Fong S, G Godowski PJ, Grimaldi J Mather JP, Pan J, Paon Williams PM, Wood WI, (GETH ) GENENTECH INC. WPI; 2003-765473/72. P-PSDB; ADB29462. syndrome. 

Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;

Length 1100; Score 1090.6; DB 9; Pred. No. 4.4e-227; 99.1**%**; 99.6**%**; Query Match Best Local Similarity

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Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Albreimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; and monetrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticosqulant.
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12-NOV-1997;
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## (GETH ) GENENTECH INC.

Perrara N;
ME, Goddard A;
Kljavin IJ; Tumas D; H, Gerritsen N Hillan KJ, R Stewart TA, Desnoyers L, E Botstein D, Desnoyers L, Fong S, Gao W, Gerber H, Grimaldi JC, Gurney AL, Pan J, Paoni NF, Roy MA, Ashkenazi A, Filvaroff E, Godowski PJ, Williams PM, Mather JP,

WPI; 2003-503392/47.

P-PSDB; ADA18318.

New secreted and transmembrane polypeptides useful for treating skin, neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and multiple sclerosis.

Claim 2; SEQ ID NO 256; 471pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating

cc at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodics are useful for modulating the biological activity of a cell expressing a PRO polypeptide. The PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastronitestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis) Parkinson's disease, Alzheimer's diseases, amyotrophic lateral scherosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides are selected to uncontrolled cell growth, e.g. cancer. PRO polypeptides are selected to uncontrolled cell growth, e.g. cancer. Cc diseases, amyotrophyle can be also used in assays to determine infection. The RRO polypeptides can be also used in sasays to determine infection. The RRO polypeptides can be also used in sasays to determine the papicy determine the read and their processes of their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with captured and other and their polymuclacides are useful in modulating endomerrial bleeding angiogenesis, and may also have an effect on kidney to solate the full-length RRO cDNA or to isolate other cDNA; including uses as hybridisation probes for changement and screening of the process and gene mapping, in the generating transgenic annuals or the reparating RRO polypeptides, for generating transgenic annuals or therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly experisely and procein and for chromosome and gene mapping, in the generating companies of the RRO polypeptide (adantses) or prevent the effect of the RRO polypeptide (adantses) or prevent the effect of the RRO polypeptide (ada 

Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;

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